Page 1

.0 1713 3 .0 1713 5 .0 2042 4 .0 2285 4	69 7.0 363 3 68.5 6.9 382 4	68 6.9 693 11 68 69 69 69 69 69 69 69 69 69 69 69 69 69	688 688 67.5 69.9 69.9	67.5 6.8 875 1 67.5 6.8 875 1 67.5 6.8 875 2	5 c/8 8.0 c./0	ALIGN	RESULT 1	US-US-UBU-383-15; Sequence 15, Application US/09080983; Patent No. 6197948; GENERAL INFORMATION:	iis	APEVINE L THEIR U	STREET: Clinton Square, P.C. Box 1 CITY: Rochester STATE: New York COUNTRY: U.S.A.	COMPUTER READABLE FORM:	MEDIUM TYPE: ALDSPY GASK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS	SOFTWARE: Patentin Release #1.0, VCURRENT APPLICATION DATA: APPLICATION NUMBER: 113/09/080 983	FILING DATE:	PRIOR APPLICATION DATA: APPLICATION NUMBER: 118 60/047 194		NAME: Goldman, Michael L.	REGISTRATION NUMBER: 30,727 REFERENCE/DOCKET NUMBER: 19603/163	TELECOMMUNICATION INFORMATION:	TELEFAX: (716) 263-1600	SEQUENCE CHARACTERISTICS:	LENGTH: 198 amino acids TYPE: amino acid	3:	; MOLECULE TYPE: protein US-09-080-983-15	Ouerv Match	Best Local Similarity 100.0%; Pred. Partches 198; Conservative 0; Misma	
ťå.		ch time 21 Seconds t alignments) Million cell updates/sec	.GGVVNTPVSNLRQLGRREVM 198			328717				* *. 	d by chance to have a the result being printed, re distribution.		Description	Sequence 15, Appl	Sequence 30074, A Sequence 2, Appli	Sequence 16, Appl	Sequence 20306. A	Sequence 32037, A Sequence 13, Appl	Sequence 6405, Ap Sequence 16, App.	Sequence 16, Appl Sequence 36, Appl	Sequence 26, Appl Patent No. 5310678	Sequence 4, Appli	Seguence 31879, A Seguence 21752, A	~ ~	Sequence 7238, Ap Sequence 4, Appl		Sequence 6918, Ap Sequence 6952, Ap	17176,
GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd	ng sw model	003, 14:47:43 ; Search til (without alid 398:931 Mill	TDASSL	Gapext 0.5	42310858 residues	chosen parameters:	0	0% 1100% 45 summaries	AA:* [ata/1/jaa/5A_COMB.pep:*	<pre>6/ptodata/lliaa/5B COMB.pep:* 6/ptodata/l/iaa/6A COMB.pep:* 6/ptodata/l/iaa/6E COMB.pep:* 6/ptodata/lliaa/PurUS COMB.pep:* 6/ptodata/l/iaa/backfilesl.pep:*</pre>	r of results predicted by cequal to the score of the rysis of the total score dis	SUMMARIES	QI	US-09-080-983-15	US-C9-252-991A-30074 US-C8-445-135-2	US-08-770-544-16 US-09-579-259-16	US-09-252-991A-20306	US-09-080-983-13	US-09-107-532A-6405 US-08-484-105-16	US-08-484-1C6-16 US-09-357-251-36	US-09-422-869-26	US-08-576-165-4	US-09-252-991A-31879 US-09-252-991A-21752	US-09-171-699-10 US-08-671-548C-46	US-09-328-352-7238 US-08-137-627-4	US-08-865-348-4 US-08-531-439B-4	US-09-107-532A-6918 US-09-107-532A-6952	US-09-252-991A-17176
Gen Copyright (c)	protein search, using	November 7, 200	US-09-613-486-15 991 1 MELMSDSNLSNLVI	BLOSUM62 Gapop 10.0 , Gap	328717 seqs, 423	hits satisfying	ength: 0 ength: 20000000000	Minimum Match Maximum Match Listing first	Issued_Pa : /cgn2_	2: /cgn2_6/ptod 3: /cgn2_6/ptod 4: /cgn2_6/ptod 5: /cgn2_6/ptod 6: /cgn2_6/ptod	is the num ter than o ived by an	ن	* Query Match Leng	100.0 198 3	732 4	0. 477 2	.8 410 4	.7 223 3	.4 706 1	.4 706 1 .4 503 3	.3 641 3	.3 707 2	.2 486 4 .2 597 4	.2 1048 4 .2 193 4	.2 1040 4 .1 359 1	.1 359 2	.1 586 4 .0 206 4	.0 414 4
	OM protein - pro	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number of	Minimum DB seg l Vaximum DB seg l	Post-processing:	Database :		Pred. No. score grea and is der		ore	1				n on	0 4	OI M	-4" LΩ	n uo l	- m	о С	7 7	w 4.	25 70.5 26 69.5	7

Sequence 10, Appl	JS-08-464-410A-10	w	875	8.9	67.5	4.5
10,	US-08-463-949A-10	7	875	6.8	67.5	44
Sequence 10, Appl	US-08-250-847B-10	-1	875	9.8	67.5	43
Sequence 10, Appl	US-08-480-547A-10	-	875	6.8	67.5	42
Seguence 4377, Ap	US-09-328-352-4377	4,	424	6.9	67.5	41
Sequence 2, Appli	US-08-596-985-2	-	911	6.9	99	40
Sequence 5, Appli	US-09-336-447A-5	4	892	6.9	68	39
Seguence 11, Appl	PCT-US95-03934A-11	Ŋ	693	6.9	68	38
Sequence 11, Appl	US-08-914-853-11	~	693	6.9	8 9	37
11,	US-08-224-917-11	~	693	6.9	68	36
11,	US-08-463-620-11	Н	693	6.9	68	35
Sequence 6865, Ap	US-09-328-352-6865	4	398	6.9	68.5	34
Sequence 4807, Ap	US-09-107-532A-4807	4	382	6.9	68.5	33
Sequence 13, Appl	US-08-984-618-13	ო	363	7.0	69	32
Sequence 2, Appli	JS-09-308-375-2	4	2285	7.C	69.5	31
Seguence 6, Appli	US-09-077-098A-6	4	2042	7.0	69.5	33
Sequence 24, Appl	PCT-US94-10261A-24	S	1713	7.0	69.5	29
Sequence 24, Appl	US-08-600-982-24	m	1713	7.0	69.5	28

S
H
7,
Θi
77
ñ
H
ы
Æ

	Gaps
S	.; o
PER PROPRIET OF STATE	100.0%; Score 991; DB 3; Length 198; Similarity 100.0%; Pred. No. 1.7e-105; 8; Conservative 0; Mismatches 0; Indels
MESULT 1 105-09-080-98 105-09-080-98 APPLICAM ATONNE MADMER	Query Match Best Local Matches 19
00 00 00 00 00 00 00 00 00 00 00 00 00	

c;

0; Gaps

```
61 TISPKVQRADSOVIFSNSFGBRNVVVTBGDLKKVLDGGAPLTRFTRKLRTFGRTFTEAYV 126
                                                                                                               DFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQOSRKMPASMYALKTESG 180
                                                                                                                                                                                                1 YELMSJSNLSNLVIIDASSLNGVJKKLLSAEVENMLVQKGAPNEGIEVVFGLLLYALAAR 60
                        APPLICANT: Sylvain Molneau, Barbara
APPLICANT: 3. Holler, Peter A. Vandenbergh,
APPLICANT: Denezer R. Vedamuthu, Jeffrey K.
APPLICANT: Ebenezer R. Vedamuthu, Jeffrey K.
APPLICANT: Chondo
TITLE OF INVENTION: DNA Encoding Phage
TITLE OF INVENTION: From Lactococcus
TITLE OF INVENTION: From Lactococcus
TITLE OF INVENTION: From Lactis, and Method of Use Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1an C. McLeod
STREET: 2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCMPUTER: Acr

COMPUTER: Acr

SOFTWARE: Mordperfect 5.1

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/08/910,551B

FILING DATE: Aquat 11, 1997

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: Ian C. NCLEOG

REGISTRATION NUMBER: 20,93:

REFERENCE/DOCKET NUMBER: 20,93:

REFERENCE/DOCKET NUMBER: 20,93:

TELEFAM: (517) 347-4103

TELEFAM: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08910551B
Patent No. 5910571
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: No FRAGMENT TYPE: N/A ORIGINAL SOURCE: ORIGINAL SOURCE: STRAIN:
                                                                                                                                                                                                                                                        181 VVNTPVSNLRÇLGRREVM 198
                                                                                                                                                                                                                                                                                 STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
DESCRIPTION: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Michigan COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okemos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                        US-08-910-551B-2
                                                                                                                                                                          121
  ò
                                          29
                                                                                       ò
                                                                                                                             g
                                                                                                                                                                       ਨੇ
                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                          ò
```

```
Patent No. 653195

Reguence No. 653195

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDCMONAS TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDCMONAS TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
REGORD NO 30034

LENGTH: 732

LENGTH: 732

LENGTH: 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ر
د ز
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 EFLNEFNLICRENNLIINDNKTKVDNFPFVDKSSKSDIFSFFENITSTN'SNDKWIKEISN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 FIDYCVNEEHLGNKGAIKCIFPVI-----TNTLKQKKVDTKNI-DNIFSKRNNYTNFN 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 ----NELIKVTKADAPAFYQGILELKGQLRRLETLGKPVVAAINGAALGGGWEICLACHH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 NSFGERNVVVTEGDLKKVIDGCAPLIRFINKLRIFGRTFIEAY------VDFCIAYKH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- ASSLNGVDK--KLLSA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 ASSINGUDKKILSAEUEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKVQRADSDVIFS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 EVEKMLVQKGAPNEG-IEVVFGLLLYALAARTTSPKVQRADSDVIFSNSFGERNVVVTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 ANTWINGVYREAMAKTIARLEAEK----EGIA---GUVL-----TSAKKTFFAGGDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
8.2%; Score 8.1; DB 4; Length 732;
Best Local Similarity 22.4%; Pred. No. 1.9;
Matches 30; Conservative 26; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.6%; Score 85; DB 2; Length 599; Best Local Similarity 24.3%; Pred. No. 0.5; Matches 36; Conservative 26; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 DLKKVLDGCAPLTRFTNKLRTFGRTFTE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 VFEXILDLSLKDSRLTNKFLTFFENINE 400
                                                                                                                                                                                                                                                                                                   KAME/KEY: phage abortive infection LOCATION: N/A LDENTIFICATION METHOD: based upon DNA OTHER INFORMATION: phage resistance OTHER INFORMATION: enzyme AbiE PUBLICATION INFORMATION: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ELMSDSNL----SNLVITD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 KLPQLNAPAELGIP 142
                                          HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL LYPE: bacterium
CELL LYPE: N/A
ORGANEILE: N/A
IMMEDIATE SOURCE:
LIBRARY: GENOMIC
CLONE: SMQ-20
                                                                                                                                                                                                        CLONE: SMQ-20
POSITION IN GENOME: N/A
                          DEVELOPMENTAL STAGE:
INDIVIDUAL ISCLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-09-252-991A-30074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-252-991A-30074
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-910-551B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ω̈́,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC
CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
Cp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Quaranta, Vito
APPLICANT: Quaranta, Vito
APPLICANT: Quaranta, Vito
APPLICANT: Quaranta, Marketta
TITLE OF INVENTION: Promotion of Epithelial Cell Adhesion
TITLE OF INVENTION: and Hemidesmosome Assembly by a Laminin-Like Molecule
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Moobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 ELLNEAKMTRKRLQÇEINPALNSLQQTLKTVSVQKDLLDAN------VTAV 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 RITSPKVQRADSDVIFSNSFGERNVV-VTEGDLKKVLDGCAPLTRFTNKLRT-FGRT--- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 RNDLRGIQRGDIDSVVS---GAKSMVRKANGITSEVLDGSAPSRRIWEGLRTATGCTRHE 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ELMSDSNLSNLVITDA--SSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%; Score 79.5; DB 1; Length 770; 26.6%; Pred. No. 3.1; tive 22; Mismatches 54; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patertin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PIOR APPLICATION DATA:
APPLICATION NUMBER: US C8/151,134
FILING DATE: 12.NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A:
REFERENCE/DOCKET NUMBER: DESXOS.002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 -FTEAYVDFCIAYK---HKLPQL 133
                                                                                                              Sequence 2, Application US/08445135 Patent No. 5658789
  144 RIALDNPGVQLGLP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.6%
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: i
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                     92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-08-445-135-2
                                                                                          US-08-445-135-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
g
```

RESULT 5 US-08-770-544-16 ; Sequence 16, Application US/08770544

```
12 LVITDASSLNGVDKKLLSAEVEKMINOKG---APNE-GIEVVFGILLYALAARTTSPKVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 ---RADSDVIFSNSFGERNVVVTEGDLKKVL----DGCAPLTRFTNKLRTFGRTFTEAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 DFCIAYKHKLPQINAAAELGIP------AEDSYLAADFLGTCPKLSELQQSRKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 DGYRVETEL-----GQKRVYLSYSEVREAILGGKYGASP----TWTVRSFMRYFAHTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
GENERAL INFORMATION:
APPLICANT: Gonsalves, Dennis
APPLICANT: 1.50
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
TITLE OF INVENTION: THEIR USES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
8.0%; Score 79; DB 2; Length 477;
Best Local Similarity 21.0%; Pred. No. 1.8;
Matches 43; Conservative 40; Mismatches 60; Indels
                                                                                                                                                                              ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
CITY: Rochester STATE: New York COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM: MEDIUM TYPE: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPATIBLE FORM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gonsalves, Dennis
Ling, Kai-Shu
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS
PROTEINS AND THEIR USES
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/621
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 FASMYALKTEGGVVNTPVSNLRQLG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452 MACAIAIKS ------ ANLRRG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSTEICATION: 435
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 6009008
FILING DATE: 21-DEC-1995
ATTOMNEY/AGENT INFORMATION:
NAME: GOLOman, Michael J.
REGISTRATION NUMBER: 30,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/09579259
Patent No. 6558953
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-579-259-16
```

-GAPNEGIEVV

39;

```
US-09-252-991A-32657

Sequence 32657, Application US/0925291A

Sequence 32657, Application US/0925291A

Sequence 32657, Application US/0925291A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT MARC J. RUBENITIED C ALD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TILE REPERBRICE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32657

LENGTH: 597
                                                                                                                                                                                                                                                                                                                                                                                                                                      99 APLTRFTNKLRTFGRTFTEAYVDFC-IAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     461 AALFRGTELLHPSGSTILEADDILCVIGHEHDLP---ALGKLFSQAPDRGLGARFFGDFV 517
                                                                                                                                                                                                                                                                                                                                       78 SGMDGLAFLRHASLSGKVHSVILSSEVDPILRQATISMIECLGLNFLGJLGKP-FSLERI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 -----GCAPLTRFTNKLRT-----FGRTFTEAYUDFCIAYKHKLPQLNAAAELGIP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 VHPSQLGSRALAENISALLTEFHLPPSSVMFEI----TFTGLISAPASSLENLVRLRIM 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 RWNHPHLGVLPPSHFLYVMETYNLVOKLFWQLFSQG-----LATRRKLAQLGQPINLAFN
                                                                                                                                                                                                                                                                                                                                                                                                  50 FGLLLYALAARTTSPK-VGRAD----SDVIFSNSFGE-----RNVVVTEGDL--KKVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 AEDSYLAADFL--GTCPKLSE--LQQSRKMFASMYALKTEGGVVNTPVSNLRQLGRREVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/09080983
Parent No. 6197948
SENERAL INFORMATION:
APPLICANT: Zhu, Hai-Ying
APPLICANT: Ling, Kai-Shu
APPLICANT: Long, Kai-Shu
APPLICANT: Gonsalves, Dennis
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS TYPE 2 PROTEINS
TITLE OF INVENTION: AND THEIR USES
NUMBER OF SEQUENCES: 23
                                                                                                                                                                           Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 77; DB 4; Length 597; ilarity 34.0%; Pred. No. 4.1; Conservative 8; Mismatches 44; Indels
                                                                                                                                                                                                                                90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 LEGDAQLS--AVASLYGLKLDG-----IDGEQALGR 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 KLSELQCSRKMFASMYALKTEGGVVNTPVSNLRQLGR 194
                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                        7 SNLSNLVITDASSLNG-VDKKLLSAEVEKMLVQK----
                                                                                                                                                                        Query Match 7.8%; Score 77.5; D
Best Local Similarity 25.0%; Pred. No. 2.1;
Matches 60; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Mismatches
                             LENGTH: 410
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT; CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-32657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 33; Conserv
                                                                                                                US-09-252-991A-20306
SEQ ID NO 20306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-09-080-983-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                              35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20306, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE PETERRORE: 107196.118
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/374,788
PRIOR APPLICATION NUMBER: US 60/374,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 ---RADSDVIFSNSFGERNVVVTEGDLKKVL----DGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 ILLIEKKIQ-PACTALAKHGVPKRFTPYCFDFALLDNRYYPADVL------KANA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 LPITEALQIN-----ARLRRLVLSKGGSQTPRDMGNMIVAMIQLFVLYSTVKNISVK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 DGYRVETEL-----GGKRVYLSYSEVREAILGGKYGASP----TNTVRSFMRYFAHTTI 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DECIAYKHKLPQLNAAAELGIP------AEDSYLAADFLGTCPKLSELQQSRKM 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 LVITDASSLNGVDKKLLSAEVEKMLVQKG---APNE-GIEVVFGLLLYALAARTTSPKVQ
                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUT TYPE: Floppy disk

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: 25-May-2000

CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.0%; Score 79; DB 4; Length 477; Best Local Similarity 21.0%; Pred. No. 1.8; Matches 43; Conservative 40; Mismatches 60; Indels
                       ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 6C09008
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 19,727
REFERENCE/DOCKET NUMBER: 19603/621
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-579-259-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 FASMYALKTEGGVVNTPVSNLRQLG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452 MACAIAIKS-----ANLRRKG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 477 amino acids TYPE: amino acid STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                          STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-20306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
328 -----YTINYIDFGWXGHLSAGLRQKLTQ----AVLALYTKDAYRIEKAVLRLC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 MEEMSGKNINHIMNAENKTETFITGIQNKQIKQEVAKLIVE----NFMKQVFDDGFFHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 ----GLLLYALAARTTSPKVQRADSDVIFSNSFGE---RNVVVTEGDLKKVLDGCAPLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 FINKLRIFGRIFTEAYVDF-----CIAYKHKIPQLNAAAELGIPAEDSY-LAADFLGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MELMSDSNLSNLVITDASS----INGVDKKLLSAEVEKMLVÇKGAPNEGIEVVF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.5%; Score 74.5; DB 4; Length 587; Best Local Similarity 22.6%; Pred. No. 7.8; Matches 43; Conservative 27; Mismatches 65; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LI, Joachim J
APPLICANT: CAVIN, Kimberly
ITILE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 DPHPGNLLFHVLTKEEQTQASR-KTETVHEKEFGSFAFRASTSAE-
                                                                   SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         NAME: ATINIELLO, PAMELA DENEKE
REGISTRATION NUMBER: 40,489
RESPERENCE/DOCKET NUMBER: GTC-012
TELECOMUNICATION INFORMATION:
TELEPAK: (781)893-5007
INFORMATION FOR SEQ ID NO: 6405:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
: NAME/KEX: misc_feature
: LOCATION: (B) LOCATION 1...587
;
: SEQUENCE DESCRIPTION: SEQ ID NO: 6405:
US-09-107-532A-6405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Enterococcus faecium
       MEDIUM TYPE: CD/ROM ISO9660
                             COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: S87 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 16, Application US/08484105; Patent No. 5589341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RINE, Jasper
POSS, Margate
MCNALLY, Francis J
LAURENSON, Patricia
HERSKOWITZ, Ira
LI, Joachim J
GAVIN, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STILLMAN, Bruce
BELL, Stephen P
KOBAYASHI, Ryuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 QQEGSFDESR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 PKLSELQQSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5589341
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-484-105-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TISPKVQRADSDVIFSNSFGERNVVVTEGJIKKVLDG-----CAPII----RFTNKLRTFG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 SISEKVKYVGS-----HTYVVDGKTYTVLDAWVFNYMKSJIKKYKRVNGLRAFC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 RTFTEAYVDFCIAYKHKLPQLMAAAELGIPAEDSYLAADF1-GTCFKLSELQQSRKMFAS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 CACEDLYLTVAPIMSERF-KTKAVGMKGLPVGKEYLGADFLSGTSKLMSDHDRAVSIVAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 LKNENYSSV---DSSRLSDSEVKEVLEKSKESFKSELASTDE--HFVYHIIFFLIRCAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 MSDSNLSNLVITDASSLNGVD-KKLLSAEVERXLVQKGAPNEGIEVVFGLLLYAL--AAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.7%; Score 76; DB 3; Length 223; 23.3%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                             SOFTWARE: Parent: Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/C80,983
                     ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REPERENCE/DOCKET NUMBER: 19603/1631
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEC ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 MYALKTE- -- GGVVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: :| |||
199 KNAVDRSAFTGG--ERKIVSLYDLGR 222
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 60/047,194
FILING DATE: 20-MAX-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6405, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 100 Beaver Street CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 223 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 23.34
Matches 48; Conservative
                                                                                  STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPCLOGY: linear MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-107-532A-6405
                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-39-080-983-13
```

ò g ò g g ò g

ò

σ

```
: 706 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) MOLECULE TYPE: protein US-08-484-106-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                   California
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                      STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          479 SRLIVVAVANTMDLPERILSNRISSRLGLSRVPFEPYTHTQLBII------IAARLEAV 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 ----APLTR------FTNKLRTFGRTFTEAYVDFCIAYKHKLPQLNAAAEL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 SNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNE----GIEVVFGLLLYALAARTTSP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFPLICANT: STILLMAN, Bruce
APPLICANT: BELL, Stephen P
APPLICANT: KOBAYSHI, Ryuji
APPLICANT: RINE, Jasper
APPLICANT: ROSS, Margit
APPLICANT: FOSS, Margit
APPLICANT: HERSKOWITZ, Ira
APPLICANT: LAJRENSON, Patricia
APPLICANT: LI, Joachim J
APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR: HOUDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.4%; Score 73.5; DB 1; Length 706; Best Local Similarity 19.3%; Pred. No. 13; Matches 43; Conservative 33; Mismatches 68; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         645 --- AE----- AKFGELILRRPEFGYVLSSLSENGVL 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 GIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGGVV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400
FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
                                                                                                   ZIP: 94111-418/
COMPUTER REDABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C8/484,105
FILING DATE:
CLASSIFICATION: 438
ATTONNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
RELEAM: (415) 494-8771
TELEFAM: (415) 494-8771
TELEFAM: (415) 494-8771
TELEFAM: (415) 494-8771
TELEFAM: 706 ATTON ACIDE:
SEQUENCE CHARACTERISTICS:
JENGTH: 706 ATTON ACIDE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 KVQRADSDVIFSNS--FGERNVVVTEGDLKKVLDGC---
        STREET: 4 Embarcadero Center, Suite 3403
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/08484106
Patent No. 5614618
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPCLOGY: linear
MOLECULE TYPE: protein
US-08-484-105-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                               COUNTRY: USA
ZIP: 94111-4187
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-484-106-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ದ್ದ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ें
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
99 ----APLTR-------FTNKLRTFGRTFTEAYVDFCIAYKHKLPQLNAAAEL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     588 EYTASPLOKVLRNLSFMOKVFLCAIVNRMRRSG--FAESYVYEVLEEAERLJRVMTTPD- 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 SNLVITDASSLNGVDKKLLSAEVEKMLVCKGAPNE----GIEVVFGLLLYALAARTTSP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 GIPAEDSYLAADFLGTCPKLSELQOSRKMFASMYALKTEGGVV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  645 --- AE-----AKFGELILRRPEFGYVLSSLSENGVL 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 KVQRADSDVIFSNS--FGERNVVVTEGDLKKVLDGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Fandu, iayo O.
APPLICANT: Schwaber, James S.
TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase
FILE REFERENCE: BE-113
CURRENT FILING DATE: 1999-07-20
EARLIER APPLICATION NUMBER: 66/093,530
EARLIER APPLICATION NUMBER: 66/093,530
EARLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 37
Query Match 7.4%; Score 73.5; DB 1; Best Local Similarity 19.3%; Pred. No. 13; Matches 43; Conservative 33; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-357-251-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-357-251-36
; Sequence 36, Application US/09357251
; Patent No. 6271441
                                                                                                                                                                                                                                                                                                                                         TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Office 97
SEQ ID NO 36
LENGTH: 503
```

us-09-613-486-15.rai

```
9
                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 FGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTE-AYVDFCIAYKHKLPQLNAAA 137
                                                                                                               134 LTDETQSILAQIKNNSHLDSIDAKILNDLKKRKLJAQGKITDFSVTKGPE--FSTDLTKL 191
                                                                                                                                                                    58 AARTTSPKVQ-RADSDVIFS-NSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRT--FGR 113
                                                                                                                                                                                                                                                                                 245 GFTEMPSNQYVETGFWNFDALY----VPQQHPARDL----QDTFYIKD-----PLTAEJFD 292
                                                                                                                                                                                                          192 ETJIJSDXVSTNAYKDLKFKPYNFNSQGVQISSGALH------PLNKVREEFRQIFFSM 244
                                                                                                                                                                                                                                                      114 TFTE----AYVD-----FCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELCQ 164
                                                                                    4 MSDSNLSNLV-ITDASSLNGVDKKLLSAEVEKMLVQKG-----APNEGIEVVFGLLLYAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 ELGIPAEDSYLAADFLGTCPKLSELQQSR------KWFASMYALKTEGGVV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peter
                                            40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bingham, Richard W.; Chambers, Philip; Emmerson, Patent No. 5310678-1
; Patent No. 5310678
; Patent No. 5310678
; Tille OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA; APPLICATION NUMBER: US/07/438,945
; RILING DATE: 17-NOV-1989
    OB 3; Length 503;
                                          74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE 2 DIABETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.3%; Score 72.5; DB 3; 25.4%; Pred. No. 15; tive 19; Mismatches 43;
ch 7.4%; Score 73; DB 3
I Similarity 24.6%; Pred. No. 9.2;
48; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS OF TREATMENT OF FILE REFERENCE: ARCD:3307 CURRENT APPLICATION NUMBER: US/05/422,969 CURRENT FILING DATE: 1999-10-21 EARLIER APPLICATION NUMBER: 60/134,175 EARLIER FILING DATE: 1999-05-13 WUMBER OF SEC ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/09422869
Patent No. 6235481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: POLONSKY, KENNETH S.
APPLICANT: HORITAMA, YUKIO
APPLICANT: COX, NAOHISA
APPLICANT: COX, NAOKY J.
APPLICANT: SREENAN, SEAMUS
APPLICANT: APPLICANT: APPLICANT: APPLICANT: GREENAN, SEAMUS
APPLICANT: HANIS, CRAIG I.
APPLICANT: HELL, GRAEME I.
                                                                                                                                                                                                                                                                                                                                                                            293 DKTYMDNIKAVHEQG 3C7
                                                                                                                                                                                                                                                                                                                                         165 SRKWFASMYALKTEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 25.48 Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Mus musculus
US-C9-422-869-26
Query Match
Best Local Similarity
Matches 48; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-422-869-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dC
                                                                                                                          qc
                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                              qq
                                                                                    ò
                                                                                                                                                                      ò
                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                 q
```

```
æ
                                                                                                                                                                                                                                                                                                                                                                   347 CTRIVTPFM----SPQIYSCLSGNTSACMYSKTEGALTTPYMTIKGSVIANCKMTTCRCV 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                             403 NPPGIISQNYGEAV-----SLIDKQSCNVLSLDGITLRLSGEFDATYQKNISIQDS 453
                                                                                                                                                                                                                                                                                    289 LPSVGNLNNMRATYLETLSVSTTRGFASALVPKVVTQVGSVIEELDTSYCIETDLDLY-- 346
                                                                                                                                                                                                                                                                                                                                58 AARTISPKVQRADSDVIPSNSFGERNVVV---TEGDLK------KVLDGCAPLT-RFT 105
                                                                                                                                                                                                                                          3 LMSDSNLSNLVITDASSLN-GVDKKLLSAEVEKMLVÇKGAPNEGIEVVF----GLLLYAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                        106 NKLRTFGRTFTEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQS
                                                                                                                                                                                              32; Gaps
                                                                                                                                                    Query Match 7.3%; Score 72; DB 6; Length 553; Best Local Similarity 24.1%; Pred. No. 14; Matches 49; Conservative 28; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        completed: November 7, 2003, 14:50:55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 RKMFASMYALKTEGGVVNTPVSN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     454 OVIITGNLDISTELGNVNNSISN 476
APPLICATION NUMBER: 885,765
FILING DATE: 15-JUL-1986
ID NO:1:
                                                                                        LENGTH: 553
                                                                                                             5310678-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search co
                                                                   SEC:
                                                                                                                                                                                                                                                                               55
                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Applisequence 2, Applisequence 2, Applisequence 16, Applisequence 16, Applisequence 13, Applisequence 13, Applisequence 13, Applisequence 14, Applisequence 26, Applisequence 26, Applisequence 21, Applisequence 21, Applisequence 21, Applisequence 21, Applisequence 21, Applisequence 21, Applisequence 4, Applisequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7238, Appli
4, Appli
4, Appli
6918, Ap
6952, Ap
                                                                                                                       7, 2003, 14:47:43 ; Search time 21 Seconds (without alignments) 398.931 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                         US-09-613-486-15
991
1 MELMSDSNLSNLVITDASSL......GGVVNTPVSNLRQLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              328717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lesued Patents_AA:*
    /cgn2 6/ptodata1/laa/5A_COMB.pep:*
    /cgn2 6/ptodata1/liaa/5B_COMB.pep:*
    /cgn2 6/ptodata1/liaa/6A_COMB.pep:*
    /cgn2 6/ptodata1/liaa/6A_COMB.pep:*
    /cgn2 6/ptodata1/liaa/AB_COMB.pep:*
    /cgn2 6/ptodata1/liaa/PcTUS_COMB.pep:*
    /cgn2 6/ptodata1/liaa/backfiles1.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-080-983-15
US-08-910-511B-2
US-08-445-135-2
US-08-770-544-16
US-09-252-991A-32657
US-09-252-991A-32657
US-09-252-991A-32657
US-09-080-983-13
US-09-080-983-13
US-09-107-532A-6405
US-09-357-251-36
US-09-422-869-26
US-09-422-869-26
US-09-422-869-26
US-09-357-251-36
US-09-357-251-36
US-09-357-251-36
US-09-357-251-36
US-09-357-251-36
US-09-357-251-36
US-09-353-351-3738
US-09-252-991A-31879
US-09-353-991A-31879
US-09-353-348-4
US-09-353-348-4
US-08-8131-4398-4
US-08-8131-4398-4
US-08-511-4398-4
US-08-511-4398-4
US-08-511-4398-4
US-08-511-4388-4
US-08-511-4388-4
US-08-511-4388-4
US-08-511-4388-4
US-08-511-4388-4
US-08-511-4388-4
US-09-107-532A-6952
US-09-252-991A-11176
                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                              328717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                     length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           November
                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.5
70.5
70.5
70.5
69.5
                                                                                                                                                                                                                                Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        991
885
81
79.5
79
77.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.5
73.5
73.5
72.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB e
Maximum DB e
                                                                                  OM protein
                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
No.
```

24, Appl 24, Appl 24, Appl 22,		Saps
seduence sed	2 PROTEINS	Length 138;
28 69.5 7.C 1713 3 US-08-600-982-24 30 69.5 7.0 1713 5 PCT-US94-10261A-24 31 69.5 7.0 2042 4 US-09-107-09BA-6 31 69.5 7.0 2042 4 US-09-308-75-0 32 69 7.0 363 3 US-08-984-618-13 33 68.5 6.9 382 4 US-08-107-52ZA-4807 34 68.5 6.9 382 4 US-08-107-53ZA-4807 35 68 6.9 693 2 US-08-463-618-13 36 68 6.9 693 2 US-08-463-618-13 38 68 6.9 693 2 US-08-463-11 38 68 6.9 693 2 US-08-24-97-11 38 68 6.9 693 2 US-08-24-97-11 39 68 6.9 693 2 US-08-24-97-1 40 67.5 6.8 875 1 US-08-35S-2 41 67.5 6.8 875 1 US-08-25C-847A-10 45 67.5 6.8 875 1 US-08-25C-847A-10 45 67.5 6.8 875 1 US-08-25C-847A-10 45 67.5 6.8 875 3 US-08-463-949A-10	ESULT 1 S-09-080-083-15 Sequence 15, Application US/09080983 Sequence 15, 39948 GENERAL INFORMATION: APPLICANT: Zhu, Hai-Ying APPLICANT: Ling, Kai-Shu APPLICANT: Consalves, Dennis TITLE OF INVENTION: GRAPEVINE LEAFROLD VIRUS TYPE TITLE OF INVENTION: AND THEIR USES NUMBERSEE: NIVENTION: AND THEIR USES NUMBERSEE: NIVENTION: AND THEIR USES CORRESPONDENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSEE: Nivention Square, Devans & Doyle LLP STREET Clinton Square, Devans & Doyle LLP STREET New York COUNTRY: U.S.A. ZIP: 14603 COMPUTER: Floppy disk COMPUTER: BER PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS	94 95: DB 3; L 80: 1.7e-105; 8matches 0;

.. Ç

```
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 KIPCINAAAELGIF 142
INDIVIDUAL ISCLATE: W1
DEVELOPRENTAL STAGE: N/A
HAPLOTYDE: N/A
TISSJE TYPE: N/A
TISSJE TYPE: Bacterium
CELL LINE: N/A
ORGANELLE: N/A
INMEDIATE SOURCE:
LIBRARY: Genomic
CLONE: SMQ-20
                                                                                                                                                              CLCNE: SMQ-20
POSITION IN GENOME: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-39-252-991A-30074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                             61 TISPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                               DFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASKYALKTEGG 180
                                                                                                                                                                      DFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGG 180
    MELMSDSNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAAR 60
                               MELMSDSNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAAR 60
                                                                                      TTSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Encoding Phage
Abortive Infection Protein
From Lactococcus
lactis, and Method of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sylvain Moineau, Barbara
APPLICANT: J. Holler, Peter A. Vandenbergh,
APPLICANT: Benezer R. Vedamuthu, Jeffrey K.
APPLICANT: Kondo
TITLE OF INVENTION: DNA Encoding Phage
TITLE OF INVENTION: From Lactococcus
TITLE OF INVENTION: From Lactococcus
TITLE OF INVENTION: Prom Lactococcus
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,551B
FILING DATE: August 11, 1997
CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/565,907
FILING DATE: December 1, 1995
ATTORNEY/AGENT INFORMATION:
NAME: 1an C. McLeod
REGISTRATION NUMBER: 20,931
REFRENCH/COCKET NUMBER: Quest 4.1-158
TELEPAN: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS (version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08910551B
Patent No. 5910571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Lactococcus lactis STRAIN:
                                                                                                                                                                                                                                                       181 VVNTPVSNLRQLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Ian C. McLeod
2190 Commons Parkway
                                                                                                                                                                                                                                                                                            181 VVNTPVSNLRQLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION: Protein
POTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO FRAGMENT TYPE: N/A ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Michigan
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okemos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-08-910-551B-2
                                                                                                                                                                    121
                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                       ò
                                            q
                                                                                    ŝ
                                                                                                                          S
C
                                                                                                                                                                    \delta
```

```
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
NUCLEIC ACID AND AMENO ACID SEQUENCES RELATING TO PSECIDOMONIAS TITLE OF INVENTION:
APPLICATION:
APPLICATION NUMBER: US,095/252,99.A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF EX ID NOS: 33.42
SEQ ID NO 36074
                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 FIDYCVNEEHLGNKGAIKCIFPVI-----TWILKQKKVDIKNI-DNIFSKRNMVINFN 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 NSFGERNVVJTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAY------VJFCLAYKH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 ----NELIKYTKADAPAFYQGILELKGQLRRLETLGKPVVAAINGAALGGGWEICLACHH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                    261 BFLNEFNLICRENNLIINDNKTKVDNPPFVDKSSKSDIFSFPENITSTNSNDKWIKEISN 320
                                                                                                                                                                                                                                                                                                                                                                                              ---- ASSLNGVDK--KLLSA 3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 ASSINGVDKKLLSAEVEXMIJVQKGAPNEGIEVVFGLLIYALAARTISPKVQRADSJVIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 ANTWNGVYREAMAKTIARLEAEK...-EGIA...-GVVL.-...-TSAKKTFFAGGDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 EVEKMINGKGAPNEG-IEVVFGILLYALAARTTSPKVGRADSDVIFSNSFGERNVVVTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.2%; Score 81; DB 4; Length 732;
Best Local Similarity 22.4%; Pred. No. 1.9;
Matches 30; Conservative 26; Mismatches 50; Indels 28; Saps
                                                                                                                                                                                                                                                      8.6%; Score 85; DB 2; Length 599; 24.3%; Pred. No. 0.5;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                . 95
                                                                                                                                                                                                                                                                                                                                                                                              2 ELMSDSNL----SNLVITD-------
                                                                                                                                                                                                                                                             Query Match 8.6%; Score 85; DB Best Local Similarity 24.3%; Pred. No. 0.5; Matches 36; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 DIKKVLDGCAPLTRFTNKLRTFGRTFTE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 VFEKILDLSLKDSRLTNKFLTFFENINE 400
                        LOCATION: N/A

LOCATION: N/A

LOCATION: N/A

LOCATION METHOD: based upon DNA

OTHER INFORMATION: phage resistance
OTHER INFORMATION: enzyme Abis

PUBLICATION INFORMATION: N/A

US-08-910-551B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30074, Application US/09252991A Patent No. 6551795
NAME/KEY: phage abortive infection LOCALION: N/A
```

us-09-613-486-15.rapb

Pag

```
(without alignments)
1172.633 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-613-486-15
991
1 MELMSDSNLSNLVITDASSD.......GGVVNTPVSNLRÇLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/NST_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_PEM_PUB_Pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_PEM_PUB_Pep:*
| cgn2_6/ptodata/2/pubpaa/NSC_NEW_PUB_PEP:*
| cgn2_6/ptodata/2/pubpaa/NSC_NEW_PUB_PEP:*
| cgn2_6/ptodata/2/pubpaa/NSO_NEW_PUB_PEP:*
| cgn2_6/ptodata/2/pubpaa/NSOB_NEW_PUB_PEP:*
| cgn2_6/ptodata/2/pubpaa/NSOB_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/NSOB_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/NSOB_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/NSOB_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/NSOB_NEW_PUB_PEP:*
| cgn2_6/ptodata/2/pubpaa/NSOB_PUBCOMB.pep:*
                                                                                                                                                                                                                                                       November 7, 2003, 14:49:54; Search time 23 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               644079
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   644079 segs, 171749292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Seguence 36, Appl	nence 37, Appl	Sequence 10721, A	Seguence 16, Appl	Sequence 16, Appl	Sequence 7808, Ap	Sequence 11789, A	Sequence 2, Appli	Sequence 10849, A	Sequence 377, App	Sequence 1385, Ap	Seguence 12518, A	Sequence 1, Appli	Sequence 13439, A	Seguence 7518, Ap
	Desci	Sec	Sec	Segn	Sec	Sec	Sec	Sec	Sec	Se	Se	Segn	Sec	Seq	Sec	Sec
	Q	US-10-138-842A-36	US-10-138-842A-37	US-09-815-242-10721	US-10-138-842A-16	US-10-039-112-16	US-10-032-585-7808	US-10-156-761-11789	JS-09-759-508B-2	JS-10-156-761-10849	US-10-205-823-377	US-09-925-301-1385	CS-10-156-761-12518	US-09-844-281-1	US-10-156-761-13439	US-10-032-585-7518
	DB	27	7	o,	12	12	12	15	10	15	15	6	5	δ	15	12
	Query Match Length DB	204	223	451	477	477	969	356	26926	292	368	399	451	833	485	1987
ø	Query Match	28.9	12.2	8.0	8.0	0 · 8	7.8	7.7	7.6	7.5	7.5	7.5	7.4	7.4	7.4	7.4
	Score	286	120.5	79	79	79	77	76.5	75	74.5	74	74	73.5	73.5	73	73
	Result No.	-1	7	n	4	ເກ	φ	7	σο	6	10	11	12	13	14	15

Sequence 2, Applia Sequence 26, Applaceunce 18, Applaceunce 18, Applaceunce 733, Applaceunc	10801	13.625	10 01 0 00 10 00 1	equence 4 equence 6 equence 1 equence 1 equence 2 equence 2
US-09-976-45 0 US-09-768-8 2 US-10-087-4 2 US-10-032-5 118-10-233-5	US-09-10-125-53-53-53-53-53-53-53-53-53-53-53-53-53	US-10-156-76 US-09-815-242 US-09-815-242 US-09-09138-62 US-09-891-21	US-10-192-584-6 US-09-932-183A- US-09-829-275-7 US-09-801-188-6 US-09-738-626-6	10-138-075-198-198-198-198-198-198-198-198-198-198
183 641 707 1119	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	522 530 530 720 833	2042 2085 363 803 1610	0 C C C C C C C C C C C C C C C C C C C
			<i></i>	
	70.5 70.5 70.5 70	0000000 0000000 00000000		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
9 F 8 6 C	2 4 4 4 6 4 6 4 6 6 6 6 6 6 6 6 6 6 6 6	1855 1855 1856 1856 1856 1856 1856 1856) W W W W W W W W W W W W W W W W W W W	0 0 0 H 0 H 0 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

67 QRADSDVIFSNSF-GERNVVVTGGDLKKVLDGCAPLTRFINKLRTFGRTFTEAYVDFCIA 125 7 SNISNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTISPKV 2; 28.9%; Score 286; DB 12; Length 264; 37.6%; Pred. No. 1.8e-24; tive 29; Mismatches 87; Indels 2 APPLICANT: GONSALDS, DENNIS
APPLICANT: LING, KAI-SHU
ITILE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
ITILE OF INVENTION: THEIR USES
FILE REFERENCE: 07678/02506
GURRENT APPLICATION NUMBER: US/10/138,842A
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 09/579,259
PRIOR FILING DATE: 1908-05-03
PRIOR FILING DATE: 1998-12-31
PRIOR FILING DATE: 1998-12-31
PRIOR FILING DATE: 1996-12-20
PRIOR PRIOR PRIOR DATE: 1996-12-20 US-10-138-842A-36
, Sequence 36, Application US/10138842A
; Publication No. US2030148390A1
; GENERAL INFORMATION: TYPE: PRT ORGANISM: Beet Yellow Virus Conservative Query Match Best Local Similarity Matches 71; Conserv US-10-138-842A-36 ે g ò

99 7.0

~

```
US-10-138-842A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             े
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
71 NVQPTSTFIKASFGGGKELYLTHGELNSFLGSQKLLEGKPNKLRCFCRTFQKDYISLRKE 130
                                             126 YKHKIPQUNAAAELGIPAEDSYLAADFIGTCPKLSELQQSRKMFASMYALKTEGGVVNTP 185
                                                                      64 ------PKVQRAD---SDVIF-SNSFGERNVVVTEGDLKKVLDGCAPLTRFTNK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 DDITGITYTREGVEVDLSDKLWTDIVYNSKGIGNR----------TNA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRTFGRTFTEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 LVITDASSLNGVDKKLLSAEVEKMLVQKG----APNEGIEVVFGLLLYALAARTTS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55;
                                                                                                                                                                                                                                                                   PUBLICATION NO. US20030148395A;
PUBLICATION NO. US20030148395A;
PUBLICANT: GONSALVES, DENNIS
APPLICANT: LING, KAI-SHU
TITLE OF INVENTION: THEIR USES
FILE REFERENCE: 07678/02506
TITLE OF INVENTION: THEIR USES
FILE REFERENCE: 07678/02506
CURRENT APPLICATION NUMBER: US 09/579,259
PRIOR APPLICATION NUMBER: US 09/579,259
PRIOR APPLICATION NUMBER: US 09/579,4898
PRIOR APPLICATION NUMBER: US 09/579,544
PRIOR FILING DATE: 1998-12-31
PRIOR APPLICATION NUMBER: US 60/009,008
PRIOR FILING DATE: 1995-12-21
NUMBER: OF SEQ ID NOS: 67
SEC ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.2%; Score 120.5; DB 12; Length Best Local Similarity 25.8%; Pred. No. 2e-05; Matches 54; Conservative 31; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 MFASMYALKTEGG--VVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-815-242-10721

Sequence 10721, Application US/C9815242

; Patent No. US2002061569A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oblsen, Kari L.
Zyskind, Uduith W.
Zyskind, Uduith W.
Zyskind, Uduith W.
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Citrus Tristeza Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari J.
                                                                                                                                                                190 VTSLKQLGR 198
                                                                                                                                186 VSNLRQLGR 194
                                                                                                                                                                                                                                                          JS-10-138-842A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-138-842A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
  g
                                                                                     Cp.
                                                                                                                                ઠે
                                                                                                                                                                       23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

us-09-613-486-15.rapb

```
LVITDASSLNGVDKKLLSAEVEKMLVQKG---APNE-GIEVVFGLLLYALAARTTSPKVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32; Mismatches
                                                                                                                                                                                                                                                        169 FASMYALKTEGGVVNTPVSNLRQLG 193
                                                                                                                                                                                                                                                                                            452 MACAIAIKS------ANLRRKG 467
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7808, Application US/10032585 Publication No. US20030180953A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME KEY: MISC FEATURE
LOCATION: (403)..(403)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 GGVVNTPVSNLRQLGRREV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---NTKLEROKSLRDKEI 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CRGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Transes 39; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-156-761-11789
                                                                                                                                                                                                                                                                                                                                                                         US-10-032-585-7808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-032-585-7808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280
                                                                                                68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΩΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D,
                                                  C.C.
                                                                                                                             Ωp
                                                                                                                                                                       ò
                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \ddot{o}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ਨੇ
                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                11;
                                                                                                                                                                                                               ---RADSDVIFSNSFGERNVVTEGDLKKVL----DGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                          354 DGYRVETEL-----GQKRVYLSYSEVREAILGGKYGASP----TNTVRSFMRYFAHTTI 403
                                                                                                                                                                       LPITEALQIN-----ARLRRLVLSKGGSQTPRDMGNMIVAMIOLFVLYSTVKNISVK 353
                                                                                                                                                                                                                                                                                          121 DFCIAYKHKLPQLNAAAELGIP-----AEDSYLAADFLGTCPKLSELQQSRKM 168
                                                                                                                                                                                                                                                                                                                                   --- KANA 451
                                                                                                                                   12 LVITDASSLNGVDKKLLSAEVEKMLVQKG---APNE-GIEVVFGLLLYALAARTTSFKVQ 67
                                                                                                  Gaps
                                                                                                62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

8.0%; Score 79; DB 12; Length 477;

Best Local Similarity 21.0%; Pred. No. 3.5;

Matches 43; Conservative 40; Mismatches 60; Indels
                                                            Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Batenin Release #1.0, Version #1.30
SOFTWARE: Patenin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/039,112
FILING DATE: 31-Dec-2001
CLASSIFICATION NUMBER: US 6009008
FILING DATE: 21-DEC-195
ATTORNEY/AGENT INFORMATION:
NAME: GOldman, Michael L.
REGISTRATION NUMBER: 19603/621
TELEPRATION NUMBER: 19603/621
TELEPRAT: (716) 263-1600
                                                                                                                                                                                                                                                                                                                             404 TLLIEKKIQ-PACTALAKHGVPKRFTPYCFDFALLDNRYYPADVL---
                                                                                            60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gonsalves, Dennis
Ling, Kai-Shu
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS
PROTEINS AND THEIR USES
                                                        DB 12;
3.5;
                                                                                              4C; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-039-112-16
                                                        Query Match 8.0%; Score 79; Best Local Similarity 21.0%; Pred. No. Matches 43; Conservative 40; Mismatc
                                                                                                                                                                                                                                                                                                                                                                       169 FASMYALKTEGGVVNTPVSNLRQLG 193
                                                                                                                                                                                                                                                                                                                                                                                                         452 MACAIAIKS-----ANLRRKG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/10039112
Publication No. US20030198942A1
GENERAL INFORMATION:
ORGANISM: Grapevine Leafroll Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIF: 14603
                    US-10-138-842A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-039-112-16
                                                                                                                                                                         302
                                                                                                                                                                                                               68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                    CC
                                                                                                                                                                                                                                                                                                                                 쉱
                                                                                                                                   င်
                                                                                                                                                                       g
                                                                                                                                                                                                               င်
                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                         q
```

11,

Gaps

62;

```
APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Garles, Boone
APPLICANT: Howard, Bussey
IITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
IITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
IITLE OF INVENTION: 9099
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEC ID NO 7808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 YDSKIIQVKELTKELEDHAR-----EIETDFL--PTITDLESKLKVXAOQ---- 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 TSPKVQRADSDVIFSNSFGER---NVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 LPITEALQIN------ARLRRLVLSKGGSQTPRDMGNMIVAMIQLFVLYSTVKNISVK 353
                                                                                                                                 ---RADSDVIFSNSFGERNVVVIEGDLKKVL----DGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                               354 DGYRVETEL-----GOKRVYLSYSEVREAILGGKYGASP----TNTVRSFWRYFAHTTI 403
                                                                                                                                                                                                                                                                   121 DFCIAYKHKLPQLNAAAELGIP-----AEDSYLAADFLGTCPKLSELQQSRKM 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ELMSDSNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 YVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.8%; Score 77; DB 12; Length 696; 19.6%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                     Sequence 11789, Application US/10156761 Ubblication No. US20303119018A1 CENERAL INFORMATION:
APPLICANT: OWUNA, SATOSHI APPLICANT: ISEDA, HARNUO APPLICANT: ISHIKAWA, JUN APPLICANT: HORIKAWA, HIROSHI APPLICANT: HORIKAWA, HIROSHI
```

```
IKEDA, HARUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-205-823-377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21588 THYIIEKRETSRLAWALIEDKCEAQSYTAIKLINGNEYQFRVSAVNKFG-VGRPLDSDPV 21646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21531 VYTVEAKNASGSAKAEIKVKVQDTPGKVVGPIRFTNITGEKMTLWWDAPLN---DGCAPI 21587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----YKHKLPQLNAAAELGIPAEDSYL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 LAARTTSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKL-RTFGRTF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 LAARHGQAWVTTGDPR-LYENGTPEQSVQAIRGQABKLADACAAIGRDVKELDKVLLTGF 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 LYALAARITS-----PKVQRADSDVI----FSNSFGERNVVTEGGLKKVLDGCAPL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21647 VAÇIQYTVPDAPGIPEPSNITGNSITLIWARPESDGG-----SEIQQYILERRE 21695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 AADFLGTCPKLSELQQSRKMFASMYAL----KTEGGVVNTPVSNLRQ--LGRRE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09759508B
Publication No. US20020182599A1
GENERAL INFORMATION:
TILLE OF INVENTION: Mark C.
TILLE OF INVENTION: Methods for Diagnosing and Treating Heart Disease FILE REFERENCE: 00786/381002
CURRENT APPLICATION NUMBER: US/09/759,508B
CURRENT APPLICATION NUMBER: US 60/175,787
PRIOR APPLICATION UMBER: US 60/175,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 TPDRGRPLESLDAFVDF--AGRH------MELGITCIAIHWPIPDSCFAAC 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 T------BAEDSYLAAD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 26926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
7.7%; Score 76.5; DB 15; Length 3
Best Local Similarity 30.1%; Pred. No. 4.4;
Matches 34; Conservative 12; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.6%; Score 75; DB 10; Length 269
Best Local Similarity 22.3%; Pred. No. 3.9e+03;
Matches 39; Conservative 27; Mismatches 67; Indels
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENION: NOVEL POLYNCULEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
FRICR FILING DATE: 2001-05-30
PRICR FILING DATE: 2001-05-30
PRICR FILING DATE: 2001-05-30
PRICR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 TRFTNKLRTFGRTFTEAYUDFCIA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-10-156-761-10849
S. Squance 10849, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
SEC ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NCS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 26926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-759-508B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-759-508B-2
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 356
```

Ω Ω ò ΩĐ

ઠે

DD.

ò

ò Ω. ò

S

```
APPLICANT: DAGO, Xumei
APPLICANT: DAGO, Xumei
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
FRIOR PLING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 GAGOFARYEAVLRKVAD-CAPVPLLVPIGERF--DVGALGRVDALLVCGGLIPAYQDALA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 ------ETBAYUDGCAPL-----TRFINKLRIFGRI------FTBAYUDFCI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 DMHTYLIGGSWDERGAEAVYGPFUBAAGQRAGR---QRAAGDAAVVGC----LLVDEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 EVEKMINQKGAPNEGIEVVFGILLYALAARTTSPKVQRADSDVIFSNSFGERNVVVTEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cuery Match
7.5%; Score 74.5; DB 15;
Best Local Similarity 28.3%; Pred. No. 5.5;
Matches 39; Conservative 12; Mismatches 48;
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHA
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: BATTORI, WASAHIRA
TILE CINVENTON: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILLOCATION NUMBER: US/10/156,761
CURRENT FILLNG DATE: 2002-05-29
FRIOR PILLNG DATE: 2001-08-02
FRIOR PLILNG DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 377, Application US/10205823
Publication No. US20030108963A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT CORGANISM: Streptomyces avermitilis US-10-156-761-10849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 AYKHKLPQLNAAAELGIP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 EVLGRLPRV--LAERGIP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoersch, Sebastian
Kamatkar, Shubhangi
Wonsey, Angela M.
Glatt, Karen
Zhao, Xumei
```

S

```
69 -ADSDVIFSNSFGERNVVVTE-------
                                                      APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIRAMA, JUN
APPLICANT: SHIRAMA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIVUK:
APPLICANT: SAKAKI, YOSHIVUK:
APPLICANT: SAKAKI, YOSHIVUK:
APPLICANT: BATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-39
PRIOR FILING DATE: 2001-05-30
PRIOR PLING DATE: 2001-05-30
PRIOR PLING DATE: 2001-06-05
PRIOR PLING DATE: 2001-06-05
NUMBER OF SEO ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Streptomyces avermitilis
US-10-156-761-12518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/0984281; Patent No. US20020082386A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 ASMYALKTEGGVVNTP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 PAYHAIATALGGTSTP 352
      Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bacillus anthracis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-844-281-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-844-281-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 DGRLVEYDIDEVVYDEDSFYQNIKILHSKQFGNIL-----ILSGDVNLAESDLAYTRAI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 -----KVLDGCAPLTRFT--NK1 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 RTFGRTFTEAYVDFCI-----AYKHKLPQLNAAABLGIPAEDSYLAADFLGTCP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 DNLKGDCYQVLIEDCIPVLKRYAKEGREFDYVINDLTAVPISTSPEEDS--TWEFLRLIL 332
                                                                                                                                                                                                                                                                                                                                                                       130 DGRLVEYDIDEVVYDEDSPYQNIKILHSKQFGNIL-----ILSGDVNLAESDLAYTRAI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                       80 -----GERNVVVTEGD-----LK-----KVLDGCAPLTRFT--NKL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 MGSGKEDYTGKDVLILGGGDGGILCEIVKLKPKMVTMVEIDQMVIDGCKKYMRKTCGDVL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 RIFGRIFIEAYVDFCI-----AYKHKLPQLNAAAELGIPAEDSYLAADFLGTCP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 DNLKGDCYQVLIEDCIPVLKRYAKEGREFDYVINDLTAVPISTSPEEDS--TWEFLRIIL 301
                                                                                                                                                                                                                                                                                                              24 DKKLLSAEVEKMLVÇKGAPNEGIEVV----FGLLLYALAARTTSPKVÇRADSDVIFSNSF 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 DKKLLSAEVEKMLVQKGAPNEGIEVV----FGLLLYALAARTTSPKVQRADSDVIFSNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1385, Application US/09925301
Patent No. US20020552308A1
GERREAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA.06
CURRENT APPLICATION NUMBER: US/05/925,301
CURRENT APPLICATION NUMBER: PCT/US00/05982
PRIOR APPLICATION NUMBER: PCT/US00/05982
PRIOR APPLICATION NUMBER: PCT/US00/05982
PRIOR APPLICATION NUMBER: PCT/US00/05982
PRIOR APPLICATION NUMBER: 60/124,270
                                                                                                                                                                                     Length 368;
                                                                                                                                                                                  Ouery Match 7.5%; Score 74; DB 15; Length 368
Best Local Similarity 22.5%; Pred. No. 8.9;
Matches 50; Conservative 36; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.5%; Score 74; DB 9; Length 399;
22.5%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 DLSMKVLKQDGKYF-----TQGNCVNLTBALSLYBEQLGR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 KLS--ELOQSRKMFASMYALKTEGGVVN-TPVSNL--RQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 DLSMKVLKODGKYF-----TOGNCVNLTEALSLYEEOLGR 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 KLS--ELQQSRKMFASMYALKTEGGVVN-TPVSNL--RQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-10-156-761-12518
; Sequence 12518, Application US/10156761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 22.54
Matches 50; Conservative
                                  ; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
US-09-925-301-1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-925-301-1385
SEQ ID NO 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ω.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>2</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \dot{c}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
```

```
10;
                                                                                                                                                             255
                                                                                                                                                                                                                                                             256 FADLGV------DVAITELDIRMQLPATDAKLTQQAADYKAVLDACVAVTRCVG-VT 305
                                                                                                                                                                                                                                                                                                                           110 TEGRTETEAYVDFCIAYKHKLPQ1NAAAELGIPAEDSYLAADFJGTCPKLSELQQSRKMF 169
                                                                                                                                                                                                                   ---GDLKKVLDGCAPLTRFTNKLR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 NISNLVITDASSINGVDKKLLSAEVEXMLVQKG----APNEGIEVVFGLLLYALAA--R
                                                                                                        10 SNLVITDASSLNGVDKKLLSA-EVERMLVQKGAPNEGIEVVFGLLLYALAARTISPKVQR
                                                                                                                                          Length 833;
                                                                                                                                                                                                                                                                                                                                                          306 VWGFTDSDSWI------PDVFSGYGAATPYDENY-----APK-
     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                     Indels
                                                     903
  DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mangold, Beverly L.
APPLICANT: Mangold, Benerly L.
APPLICANT: Aldrich, Jennifer L.
APPLICANT: O'Brien, Thomas Specific Antibodies
TILE REFERENCE: 38672.003
CURRENT APPLICATION NUMBER: US/09/844,281
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 60/200,505
PRIOR APPLICATION NUMBER: 60/200,505
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.4%; Score 73.5; DB 9; Best Local Similarity 24.7%; Pred. No. 34; Matches 53; Conservative 29; Mismatches 90;
Query Match 7.4%; Score 73.5; DB Best Local Similarity 21.4%; Pred. No. 14; Matches 42; Conservative 33; Mismatches
```

```
782
                                                                                                                                                                                                                                                                                                                                                                                                            -----RFTNKL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                  783 VDNI------NAEIVAGSITTIEEGIEWLTYTYFFVRWLQSPALYGVEATYDFINDP 833
                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 RTFGRIFTEAYVDFCIAYKHKIPQLNAA-----ABLGIPAEDSYLAADFLGTCPKLSEL
                                                                                                                                                                                                                                                                                                                         21 NGVDKKLLSAEVEKMLVQKGAP-----BUTI-----EVVFGLLLYALAARTTSPKVQRA
                                                                                                                                                                                                                                                                                                                                                    834 TLYNRRADLIYTAPCILHENKLVVYNAALGSVASTELGKIASHFYINFETINLYGRMLKP
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                        Length 1987;
                                                                                                                                                                                                                                                                                88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            70 DSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 QOSRKMFASMYALKTEGGVVNTPVSNLRQLGRREV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   894 WHSETDILSVFS--NSGEFKYVPV---RQEERLEI 923
                                                                                                                                                                                                                                    Cuery Match

7.4%; Score 73; DB 12;
Best Local Similarity 21.4%; Pred. No. 1.4e+02;
Matches 46; Conservative 29; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7, 2003, 14:55:17
FILE REFERENCE: 10182-005-999
CURRENT PELLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 75:8
LENGTH: 1987
                                                                                                                                                 ; TYPE: PRT; ORGANISM: Candida albicans
US-10-032-585-7518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: November
Job time : 30 secs
                                                                                                                                                                                                                                                                                                                                                               D,
                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                             D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

Arabidopsis thalia Arabidopsis thalia Putative P. abyssi Phage abortive inf GLRAV-5 coat prote

GLRAV.5 coat prote
Erystpelothrix rhu
Erystpelothrix rhu
Erystpelothrix rhu
Erystpelothrix rhu
Lactococcus lactis
Streptcoccus poly
Streptcoccus poly
Streptcoccus poly
Rat hamidesmosome
Propionibacterium
Enterococcus faeca

AAG20733 AAG39165 AAG39165 AAN17788 AAN17788 AAN2690 ABB0787 ABB29995 ABB29995 ABB29995 AAN26787 AAN3678 AAN3678 AAN3678

Grapevine leafroll Drosophila melanog Lactococcus lactis Candida albicans e Nove: human secret Grapevine leafroll NADH oxidase Amp

```
86
84
84
85
85
81
80
80
                                                                                                                                                                                             79.
Sugar beet yellows
C. albicans BAX-as
Herbicidally activ
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Herbicidally activ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grapevine leafroll
                                                                                                            ; Search time 41 Seconds
(without alignments)
765.533 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Ceneseq_15Jun03:*

| SIDS1/gcgdata/geneseq/geneseqp_embl/AA1980.DAT:*
| SIDS1/gcgdata/geneseqy_embs_cap_embl/AA1981.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA1981.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA1983.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA1983.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA1985.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA1985.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA1985.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA1980.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA1991.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA1991.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA1991.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA1992.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA2022.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA2022.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA2022.DAT:*
| SIDS1/gcgdata/geneseqy_embl/AA2022.DAT:*
                                                                                                                                                                                                          1 MELMSDSNLSNLVITDASSL........GGVVNTPVSNLRQLGRREVX 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                              1107863
             5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                            hits satisfying chosen parameters:
             version 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                         Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                              14:44:53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW73482
AAR72682
ABB91963
AAG20735
AAG20735
AAG20734
AAG39166
ABB91962
                                                                               sw mode]
                                                                                                                                                                                                                                                                                             1107863 seqs, 158726573
                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
             GenCore (c) 1993
                                                                               បនរំពន្ធ
                                                                                                            2003,
                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
                                                                                                                                                                        US-09-613-486-15
991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٦,
                                                                             protein search,
                              Copyright
                                                                                                              Nevember
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing:
                                                                                                                                                                                                                                                                                                                            Total number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           991
286
286
36.5
86.5
86
86
86
                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                             Scoring table:
                                                                               ī
                                                                             OM protein
                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
No.
                                                                                                              on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 M 4 W 0 L 8 0
                                                                                                            Run
```

696 23 ABP73971	200 22 AAU30541 223 20 AAW73481	509 15 AAR47583	606 20 AAY43219 E. rhusiopathi	358 23 ABB91943 Herbicidally 3 404 23 ABP25433 Streptococcus	883 22 AAM51651	26926 22 AAU05396 Human titin (c	31267 24 ABG74786	445 22 AAB46239 1604 11 AAB46451	1725 21	359 23 ABB91946	399 21 AAB43940	332 21 AAG10781	7.4 355 21 AAG10780 Arabidopsis thalia		ALIGNMENTS		standard; Protein; 198 AA.		(first entry)	leafroll virus type 2 coat protein.	clant	nce, virus resistance; beet yellows	rus; coat protein.	leafroll virus type 2.	i		, 98WO-US10313.	; 97US-0047194.	CORNELL RES FOUND INC.	, Ling K, Zhu H;	45307/04. 08870.	eafroll virus (type 2) proteins and polypeptides - and
7, 7,	76	75.5	75.5	۲/ ر ۲	27.	7.5	75		. 4. . 6.	74	74	73.5	73.5)		r 1	73482	AAW73482;	29-MAR-1999 (Grapevine leaf	GRLaV-2: clost	disease resist	tristeza virus;	Grapevine leaf	WO9853055-A1.	26-NOV-1998.	20-MAY-1998;	20-MAY-1997;	(CCRR) CORNEL	Gonsalves D,	WPI; 1999-045307/04 N-PSDB; AAV08870.	Grapevine leafroll
28	9.0	31	32	an ta	35	36	W. C.	200	J 44	4	42	43	কা ধা কা ধা	•		RESULT	▼) `~												, 45 45 54 54 54 54 54 54 54 54 54 54 54 5	-		

```
32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD.
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : MELMSDSNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAAR 60
                                                                   This is the amino acid sequence of a 22 kDa coat protein that is encoded by open reading frame ORF6 (see AAV08875) of grapevine leafforl vitus type 2 (GLSAV-2) RNA (See AAV08875) of grapevine coat proteins 4 (See AAV08864-72) for a genome includes 9 open reading frames (see AAV08864-72) for a polyprotein, an RNA-dependent RNA polymerase, heat shock proteins, coat proteins of unknown function (see AAW7746-84). These can be used to produce antibodies useful for detecting GLRAV in samples e.g. by ELISA (claimed). The nucleic acid molecules can be used to produce probes and primers for such molecules can be used to produce probes and primers for such cuties, agrobacterium tumefaciens, grape, citrus, beet or tobacco citris, agrobacterium tumefaciens, grape, citrus, beet or tobacco citrian and produce transgenic plants (claimed). Hey can be used to impart GLRAV-2 resistance to vitis scion or roctstock cultivars or tristeza vitus resistance to citrus scion cultivar/rootstock cultivars (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
encoding DNA, useful e.g. to impart grapevine leafroll resistance grape and tobacco plants and detect grapevine leafroll virus
                                                                                                                                                                                                                                                                                                                                                                                                                        .
.
                                                                                                                                                                                                                                                                                                                                                                                            Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugar beet yellows virus capsid protein; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 991; DB 20; 100.0%; Pred. No. 2.4e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugar beet yellows virus capsid protein
                                           Claim 12; Page 44-45; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR72682 standard; Protein; 204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVNTPVSNLRQLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BIOT=) BIOYRCHN INST CO LTD (IMMU=) IMMUNOBIOTECHN INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91SU-4950054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9187-4950054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Love.
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugar beet yellows virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (nbdated)
                                                                                                                                                                                                                                                                                                                                                              198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RJ2017820-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR 72682;
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  े
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                           X5555666666666666666
```

```
?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 ORADSDVIFSNSF-GERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bax, Bax-resistance, cytostatic, fungicide, immunosuppressive, virucide, vasorropic; vaccine, gene therapy, proliferative disorder, cancer, apoptosis, fungal, yeast, infection, autoimmune disease, ischaemia; neurodegeneration, cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.0
                                                                                                                                                                                                                                                The amino acid sequence of the novel sugar beet yellows virus (SBYV) capsid protein. The protein has mol. wt. 22.2 kD. The corresponding gene was obtained from reverse transcribed RNA isolated from purified SBYV. The fragment is useful for the production of virus resistant transgeric plants by genetic engineering methods. ("Jpdaced on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ATFENVSLADOTCLHGEDCDKLRKNFEECLKLKGVPEDNIGIALGLCLYSCATIGTSNKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 NVQPTSTPIXASPGGGKELYLTHGELNSFLGSQKLLEGKPNKIRCFCRTFQKDYISLRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 SNLSNLVITDASSLNGVDKKLLSAEVERYLVQKGAPNEGIEVVFGLLLYALAARTISPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                            Sugar beet yellows virus cDNA fragment encoding capsid protein useful for production of virus-resistant transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eberhardt I, Luyten WHML, Reekmans RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C. albicans BAX-associated protein fragment SEQ ID 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.9%; Score 286; DB 16; 37.6%; Pred. No. 6.2e-23; iive 29; Mismatches 87;
Karasev AV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG93273 standard; Protein; 499 AA.
                                                                                                                                                                                                     Claim 1; Column 7-10; Spp; Russian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-2000, 2000EP-0870318.
04-JAN-2001, 2001EP-0870002.
09-JAN-2001, 2001EP-0870003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-DEC-2001, 2001WO-EP15398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arganovskii AA, Boiko VP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CANC ) CANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 VSNIRCLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 VTSIKOLGR 198
                                                WPI; 1995-113715/15.
N-PSDB; AAQ87853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-667002/71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WJ200264766-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contreras RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-VOV-2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG93273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG93273
```

```
28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.
 ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                     preparing a medicament for treating, preventing and/or alleviating diseases associated with yeast or fungi or proliferative disorders, such as cancer, or for preventing apoptosis in certain diseases. The compounds or polypeptides, or the genetically modified organism are useful for preparing a medicament for modifying the endogenic flora of humans and other mammals. The vaccine is useful for immunising against yeast or fungal infections. Apoptosis-related diseases include autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMASWKLGPVJATGSTTVLKTAESTPLSALYLSQLLVEAGMPKGVINIVSGFGATAGAAI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 FTEAYV------DFCIA-----YKHKLPQLNAAAE---LGIP-AEJSYLAADFL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 IONIIVSIFYNSGEVCCAGSRILIGSGVYDQVVEKFKEAAESVKVGNPFDEDIFYGA--- 343
                                                                                                                                                              This invention describes a novel nucleic acid representing a synthetic Bax gene. The Bax gene of the invention is useful for identifying Bax-resistant yeast or fungl, identifying, or obtaining and identifying Candida spp. sequences that are differentially expressed in a pathway eventually leading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax-induced cell death. The products of the invention have cytostatic, fungicide; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The isolated nucleic acids, polypeptides, pharmaceutical compositions, antisense molecules and antibodies are useful as medicaments or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LMSDSNLSNLVITDASS-LNGVDKKLLSA-EVEKMLVQKGAPNEGIEVVFSLLLYALAAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ischaemia, diseases related with viral infections or neurodegenerations. This sequence represents a polypeptide associated with the Bax gene described in the disclosure of the invention.
                         New isolated nucleic acid representing a synthetic Bax gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in certain diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ITSPKVQRADSDVIFSNSFGERNVVV---TEGDLKKV---LDGCAPLIRFINKLRTFGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AKHPKIEK----VAFTGSTATGKIIMKLAAESNLKKVTLELGGKSPNIVFND--ADLDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.0%; Score 89.5; DB 23; Best Local Similarity 25.1%; Pred. No. 0.82; Matches 53; Conservative 39; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herbicidally active polypeptide SEQ ID NO 1174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---- QVSDVQLS-KILKYVESGKSQGATVVT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCPKLSELÇQSRKMFASMYALKTEGGVVNT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herbicidal, plant, agriculture, herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                 Claim 36; Figure 2; 344pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB91963 standard; Protein; 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-AUG-2001; 2001WC-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200210210-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB91963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB91963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 LSDQDILTGVCFASAGIVGDKKAMEIINNAFVVVSAGPND----FILNYYDIPSRRLEY 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 KVQRADSDVIPSN-----SFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEAYVOFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYAL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 LEHHNKDSVLYNEKLOKLILPQIEASLPG-SKFLYADVYN--PMMEMIQNPSK----YGF 266
                                                                                                                                                                                                                                                                                                                                                                   The invention relates to identifying target proteins (ABS90797-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter
                                                                                                                                                                       Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 PFISGYQDFILKRLENFVRELYSLGVRNVLV.-GGLPPM--GGLPI-HMTAKFRNIFRFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 IIDASSLNGV-----DKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 328;
                                                                                                                                                                                                                                                                                                                Claim 5; SEQ ID NO 1174; 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 23037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.7%; Score 86.5; DB 25.8%; Pred. No. 0.96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG20735 standard; Protein; 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2000; 2000EP-0301439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0121825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0123180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-0CT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 25.8%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-TEGGVVNT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KETKRGCCST 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       termination sequence
                                                                                                                WPI; 2002-269010/31
                                                      Weidler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 AA;
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-2000.
                                                         Tietjer K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116
                                                                                                                                                                                                                                                               organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG20735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG20735
```

305-3125788 305-0126264 305-0126785 905-0127462 905-0128714 905-0128714	905.01305.01 905.01305.01 905.0130891 905.0132486 905.0132486 905.0132486 905.0132486 905.0132486 905.0134219 905.0134219 905.013613286 905.01361328 905.01361328 905.01361328 905.01361328 905.01361328 905.01361328 905.0136138 905.0137528 905.0137528 905.0137538 905.0137538 905.0137538 905.0137538 905.0137538 905.0137538 905.0137538	990S-0139455. 990S-0139455. 990S-0139455. 990S-0139456. 990S-0139456. 990S-0139456. 990S-0139466. 990S-0139466. 990S-0139461. 990S-0139461. 990S-0139461. 990S-0139461. 990S-0139461. 990S-0139462. 990S-0140354. 990S-0140354. 990S-0140354. 990S-014205. 990S-014205. 990S-014205. 990S-014205. 990S-014205. 990S-014203. 990S-014203. 990S-014203.
5-MAR-1999 5-MAR-1999 5-MAR-1999 1-APR-1999 5-APR-1999 6-APR-1999	3. APR-1999 3. APR-1999 3. APR-1999 3. APR-1999 3. APR-1999 3. APR-1999 3. MAY-1999 4. MAY-1999 4. MAY-1999 5. MAY-1999 5. MAY-1999 5. MAY-1999 5. MAY-1999 5. MAY-1999 6. MAY-1999 7. MAY-1999	16-CTN-1999; 16-CTN-1999; 18-CTN-1999; 18-CTN-1999; 18-CTN-1999; 18-CTN-1999; 18-CTN-1999; 18-CTN-1999; 18-CTN-1999; 18-CTN-1999; 18-CTN-1999; 18-CTN-1999; 18-CTN-1999; 23-CTN-1999; 23-CTN-1999; 24-CTN-1999; 25-CTN-1999; 26-CTN-1999; 27-CTN-1999; 28
44 44 44 44 44 44 44 44 44 44 44 44 44	2	• • • • • • • • • • • • • • • • • • •

905.0144096 905.0144396 905.0144331 905.0144332 905.0144333 905.0144335 905.0144335 905.0144884 905.0144884 905.0144884 905.0144884	9935 0145080 995 0145080 995 0145080 995 0145145 995 0145218 995 0145918 995 0145918 995 0145918 995 0145918 995 014798 995 014798 995 014793 995 0147192 995 0147192 995 0147193	990'S-01481319 990'S-01481319 990'S-01483419 990'S-0148684 990'S-0149368 990'S-0149722 990'S-0149722 990'S-0149723 990'S-0149723 990'S-0149723 990'S-0149723 990'S-0149723 990'S-0149723 990'S-0149723 990'S-0149723 990'S-0150'S-0 990'S-015139 990'S-015307 990'S-015307 990'S-015307 990'S-015307 990'S-015307 990'S-015307 990'S-015303
16-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 20-JUL-1999 20-JUL-1999 21-JUL-1999 21-JUL-1999	22-40L-1999 23-40L-1999 23-40L-1999 23-40L-1999 24-40L-1999 27-40L-1999 27-40L-1999 27-40L-1999 27-40L-1999 28-40C-1999 02-AUG-1999 04-AUG-1999 06-AUG-1999 06-AUG-1999 06-AUG-1999	10-7400 11-740
<u>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~</u>	\$ 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	K K K K K K K K K K K K K K K K K K K

Ś

```
99US - 0.121625.
99US - 0.121626.
99US - 0.125188.
99US - 0.125188.
99US - 0.12518146.
99US - 0.12624.
99US - 0.127462.
99US - 0.128144.
99US - 0.128148.
99US - 0.13081.
99US - 0.13248.
99US - 0.134219.
99US - 0.13444.
99US - 0.13444.
99US - 0.13445.
       25-FEB-2000; 2000EP-0301439
                                       25-FEB-1999

05-KAR-1999

23-KAR-1999

25-KAR-1999

25-KAR-1999

20-APR-1999

06-APR-1999

06-APR-1999

06-APR-1999

19-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

30-APR-1999

30-APR-1999

30-APR-1999

30-APR-1999

30-APR-1999

4-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                    05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
C7-MAY-1999;
11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 - XAY - 1999
14 - MAY - 1999
14 - MAY - 1999
16 - MAY - 1999
18 - WAY - 1999
20 - MAY - 1999
21 - MAY - 1999
22 - MAY - 1999
25 - MAY - 1999
25 - MAY - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAY-1999;
C1-JUN-1999;
O3-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-1999;
10-JUN-1999;
10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1999;
02-JUL-1999;
06-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :8-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-1999
       \frac{d}{d} \sum_{i=1}^{N} \frac{d}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 SEQPNYFKSYIARLKGIVGOKKAMEIINNAFVVVSAGENDFILNYYEIPSRRLEYPFISG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAFLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 YQDFILKRLENFVRELYSLGVRNVLV--GGLPPM--GCLPI-HMTAKFRNIFRFCLEHHN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DECIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKAFASYYALK-TEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 KDSVLYNEKLONLLPQIEASLPG-SKFLYADVYN--PMMEMIONPSK-----YGFKETKR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 SNLSNLVITDASSLNGV--DKKLLSAEVENNJVQKGAPNEGI----EVVFGILLYALAAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

8.7%; Score 86; DB 21; Length 29

Best Local Similarity 26.5%; Pred. No. 0.94;

Matches 49; Conservative 23; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 48421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG39167 standard; Protein; 295 AA
99US-0158029.
99US-0158232.
99US-0158236.
99US-0159294.
99US-0159294.
99US-0159294.
99US-0159330.
99US-0159330.
99US-0159330.
99US-0159330.
99US-016074.
99US-0160767.
99US-0160767.
99US-0160767.
99US-0160767.
99US-0160767.
99US-0160768.
99US-016098.
99US-016098.
99US-016098.
99US-016098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GWWT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCGT 243
                   08-0CT-1999;
13-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
12-0CT-1999;
12-0CT-1999;
12-0CT-1999;
12-0CT-1999;
13-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG39167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG39167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
9905-0142920

9905-0143977

9905-0143624

9905-0144005

9905-0144006

9905-0144031

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0144331

9905-0147302

9905-0149330

9905-0149330

9905-01513330

9905-01513330

9905-01513330

9905-01513330

9905-0151333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-AUG-1999;

11.-AUG-1999;

13.-AUG-1999;

13.-AUG-1999;

16.-AUG-1999;

20.-AUG-1999;

20.-AUG-1999;

21.-AUG-1999;

22.-AUG-1999;

23.-AUG-1999;

23.-AUG-1999;

24.-AUG-1999;

25.-AUG-1999;

26.-AUG-1999;

27.-AUG-1999;

27.-AUG
09-JUL-1999)
12-JUL-1999
14-JUL-1999
15-JUL-1999
15-JUL-1999
16-JUL-1999
19-JUL-1999
19-JUL-1999
19-JUL-1999
19-JUL-1999
19-JUL-1999
20-JUL-1999
20-JUL-1999
21-JUL-1999
22-JUL-1999
```

\$\frac{\pi}{\pi} \\ \text{\tex

|--|

<u>α</u> , <u>α</u> , (<u>a. a.</u>			. 0. 0. 0.
		01439.	0.121180 0.121180 0.1226244 0.1226244 0.1226244 0.1226244 0.1226244 0.122624 0.132626 0.132626 0.132626 0.132626 0.132626 0.132626 0.132626 0.132626 0.132626 0.132626 0.132626 0.132626 0.132626 0.132626 0.132626 0.132626 0.132626 0.132626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626 0.133626	40823. 40991. 41287.
		0EP-03	20. 8. 1. 8.	-506 -506
-A2.	. 00	000, 250	######################################	
033405	SEP-200	FEB-20		1444
2 N	-90	ж - 25-	20 0 0 0 0 0 0 0 1 1 2 2 2 2 2 2 2 2 2 2	3.22
2 2 2	4 E. S	4 <u>G</u> 8		2 2 2

PR 01-705-1999; 9905-0141842 PR 02-705-1999; 9905-0142055 PR 06-705-1999; 9905-0142055 PR 12-705-1999; 9905-0142055 PR 12-705-1999; 9905-0142070 PR 12-705-1999; 9905-0142070 PR 12-705-1999; 9905-0144088; 9805-014408; 980 ω

```
99US-0140353
                             Arabidopsis thaliana
                                                                                                        23 - MAR - 1999)
25 - MAR - 1399)
01 - APR - 1399)
06 - APR - 1999)
06 - APR - 1999)
19 - APR - 1999)
23 - APR - 1999)
23 - APR - 1999)
                                                                                                                                                                                                        -XAY-1999;
-XAY-1999;
-XAY-1999;
-XAY-1999;
-XAY-1999;
                                                                                                                                                                                                                                                                                                                                    - JUN-1999;
- JUN-1999;
- JUN-1999;
- JUN-1999;
- JUN-1999;
- JUN-1999;
                                           EP1033405-A2
                                                                       25-FEB-2000;
                                                                                                                                                                      -MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                666
                                                                                                                                                                                                                                                                                                                                                                                             6661
                                                                                                                                                                                                                                                                                                                                                                                                    666
                                                         06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-19
18-JUN-19
18-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                              8-553N-1
                                                                                                                                                                                                                -XAY-1
                                                                                            MAR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-1
18-JUN-1
18-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                            - NDS
                                                                                                                                                                                                         -XAY-1
                                                                                                                                                                                                                                                                                    -MAY-1
                                                                                                                                                                                                                                                                                            MAY-1
MAY-1
MAY-1
                                                                                                                                                                                           0-APR-
                                                                                                                                                                                                                                            1-MAY-
                                                                                                                                                                                                                                                    -MAY-
  Ġ
                                                                                                                                                                                                                                                                                                                                        KDSVLYNEKLGNLLPQIEASLFG-SKFLYADVYN--PMMEMIQNPSK----YGFKETKR 303
                                                                                                                                                                                                                                                                                                                                                          TTSPKVQRADSOVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                                    DFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALK-T5G 179
                                                                                                                                                                                                                                                                                                                                                                  197 YQDFILKRLENFVRELYSLGVRNVLV--GGLPPM--GCLPI-HMTAKFRNIFFRCLEHEN
                                                                                                                                                                                                                                                                                                                             SNLSNLVITDASSLNGV--DKKLLSAEVEKMLVQKGAPNEGI----EVVFGLLLYALAAR
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                  8.7%; Score 86; DB 21; Length 360;
26.5%; Pred. No. 1.2;
tive 23; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 48420
                                                                                                                                                                                                                                                                                                               93 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG39166 standard; Protein; 360 AA
99US-0154039.
99US-015479.
99US-0155486.
99US-0155486.
99US-0155486.
99US-0155486.
99US-0155486.
99US-0155486.
99US-0157117.
99US-015929.
99US-0160741.
99US-0160741.
99US-0160741.
99US-0160741.
99US-0160741.
99US-0160741.
99US-0160741.
99US-0160741.
99US-0160741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                  Guery Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                GWWNT 184
                                                                                                                                                                                                                                                                                                                                                                                                                              30CCGT 308
16.52P-1999
22.5EP-1999
23.5EP-1999
24.5EP-1999
28.5EP-1999
29.5EP-1999
29.5EP-1999
20.50CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-0CT-2000
                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG39166;
                                                                                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                   252
                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                              304
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT B
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG39166
                                                                                                                                                                                                                                                                                                                                                                                                g
 q
                                                                                                                                                                                                                                                                                                                                                                      QC.
                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                             qC
                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                         8
```

```
Why Price in identification, signal remanduction pathway; metabolic pathway; we termination sequence.

XX Arabidopsis thaliana.

XX Exploses.

XX Exploses.
```

σ

```
99US-C140354.
99US-C140695.
99US-C140692.
99US-C14184.
99US-C142184.
99US-C142184.
99US-C142390.
99US-C142390.
99US-C14230.
99US-C14230.
99US-C14230.
99US-C14320.
99US-C144008.
99US-C144086.
99US-C144086.
99US-C144086.
99US-C1444086.
99US-C1444086.
99US-C1444086.
99US-C144432.
                                                                                                                                                                                                                                                                                                                                                99US - 0144335

99US - 01443484

99US - 01448814

99US - 01448814

99US - 0145088

99US - 0145087

99US - 0145087

99US - 0145087

99US - 0145192

99US - 0145145

99US - 0145145

99US - 014524

99US - 0145318

99US - 0146389

99US - 014726

99US - 0146884

99US - 0149175

99US - 015066

99US - 015066

99US - 015066

99US - 0151066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-AUG-1999)
12-AUG-1999)
13-AUG-1999)
13-AUG-1999)
16-AUG-1999)
16-AUG-1999)
20-AUG-1999)
23-AUG-1999)
23-AUG-1999)
25-AUG-1999)
27-AUG-1999)
27-AUG-1999)
27-AUG-1999)
27-AUG-1999)
27-AUG-1999)
27-AUG-1999)
27-AUG-1999)
23 - JUN - 1999;
24 - JUN - 1999;
28 - JUN - 1999;
29 - JUN - 1999;
30 - JUL - 1999;
01 - JUL - 1999;
06 - JUL - 1999;
06 - JUL - 1999;
12 - JUL - 1999;
13 - JUL - 1999;
14 - JUL - 1999;
15 - JUL - 1999;
16 - JUL - 1999;
```

```
61 TISPKVORADSDVIPSNSFGERNVVVTEGDLKKVLDGCAPLIRFINKLRTFGRIFTEAYV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12] DECIAYKHKLPOLNAAAELGIPAEDSYLAADFLGTCFKLSELQOSRKMFASMYALK-TEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 KDSVLYNEKLQNLLPQIEASLPG-SKFLYADVYN--PAMEMIONPSK-----YGFKETKR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 YQCFILKRLENFVRELYSLGVRNVLV--GGLPPM--GGLPI-HWTAKFRNIFRFCLEHHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 SNLSNLVITDASSLNGV--DKKLLSAEVEKMLVQKGAPNEGI----EVVFGLLYALAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 8.7%; Score 86; DB 21; Length 360; 1 Similarity 26.5%; Pred. No. 1.2; 49; Conservative 23; Mismatches 93; Indels
99US - 0151930.
99US - 0151930.
99US - 0153070.
99US - 0153070.
99US - 0153070.
99US - 0153070.
99US - 0154779.
99US - 0155659.
99US - 0155659.
99US - 0155659.
99US - 0155659.
99US - 0159293.
99US - 0159293.
99US - 0159293.
99US - 0159293.
99US - 0159294.
99US - 0159295.
99US - 0159296.
99US - 0159296.
99US - 016076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVVNT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGT 308
01-SEP-1999, 10-SEP-1999, 13-SEP-1999, 13-SEP-1999, 26-SEP-1999, 26-SEP-1999, 28-SEP-1999, 28-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Sest Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB91962
ID ABBS
XX ABBS
    Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

09

ABB91962 standard; Protein; 360 AA.

ABB91962,

```
121 DFCIAYKHKLPQLNAAABLGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALX-TEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 SEQPNMFKSYIARLKGIVGDKKAMEIINNAFVVVSAGPNDFILNYYEIPSRRJEYPFISG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to identifying target proteins (ABB94316) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences having an using suitable search parameters, where plant sequences having an E-value sequences are selected of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 KDSVLYNEKLQNLLPQIEASIPG-SKFLYADVYN--PMMEMIONPSK-----YGFKETKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 SNISNLVITDASSLNGV--DKKILSAEVEKYLVQKGAPNEGI----EVVFGLILYALAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TISPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRIFTEAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 YODFILKRLENFVRELYSLGVRNVLV - GGLPPM - GCLPI - HYTAKFRNIFRFCLEHHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.7%; Score 86; DB 23; Length 360; larity 26.5%; Pred. No. 1.2; Conservative 23; Mismatches 93; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; SEQ ID NO 1173; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 23035
                                                           Herbicidally active polypeptide SEQ ID NO 1173.
                                                                                                                   Herbicidal, plant, agriculture, herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG20733 standard; Protein; 366 AA.
                                                                                                                                                                                                                                                                                                                                                        28-AUG-2001; 2001WC-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                 28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
(first entry)
                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tietjen K, Weidler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GWNT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 GCCGT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FARB ) BAYER AG
                                                                                                                                                                                                                                    WC200210210-A2
31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2000
                                                                                                                                                                                                                                                                                                07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG20733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG20733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         압
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \ddot{\circ}
```

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                         990S-0131449-990S-01312048-990S-0132485-990S-0132485-990S-0132486-990S-0132486-990S-0132485-990S-0134219-990S-013458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139450-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-0139458-990S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             990S-0139750.
990S-0139763.
990S-0139817.
990S-0139899.
                                                                                                                                                                     99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
                                                                                                                                                                                                                                             990S-0126785.
990S-0127462.
990S-0128234.
990S-0128714.
990S-0129845.
                                                                                                                                                                                                                                                                                                                                 99US-0130449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0139461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0139462
99US-0139463
                                                                                                                                            2000EP-0301439
                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-1999;
22-JUN-1999;
23-JUN-1999;
                                                                                    EP1033405-A2
                                                                                                                                            25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                               666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8-JUN-1999
                                                                                                                 36-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                      APR-195
0-APR-196
30-APR-19
04-WAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8-JUN-19
8-JUN-1
                                                                                                                                                                                                                                               MAR-1
APR-1
APR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8-JUN-1
6-JUN-1
8-JUN-1
8-JUN-1
                                                                                                                                                                                                                                                                                                                                                  APR-1
                                                                                                                                                                                                                                                                                                                                   APR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -XAX-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-NJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04 - CUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                      -YAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -YAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -4-JUN-
                                                                                                                                                                                                                                                                                                      APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -KU5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7-JUN-
                                                                                                                                                                                                                                                                                         -APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -XAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -NOS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΜAΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      į
                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY
```

251

2C;

99US-0140354.

23-JUN-1999;

28

990S-0140595. 990S-0140695.	9US-0140823 9US-0140991	9US-0141287	9US-0141842 9US-0142154	9US-0142055	9US-0142390 9US-0142803	9US-0142920	90S-0142977 90S-0143542	9US-0143624	9US-01440US 9US-0144085	9US-0144086	9US-0144325 9US-0144331	9US-0144332	9US-0144333 9US-0144334	9US-0144335	9US-0144632	9US-0144884	9US-0144814 9US-0145086	9US-0145088	9US-0145087	9US-0145089	908-0145192 908-0145145	9US-0145218	9US-0145224	9US-U145276 9US-0145913	9US-0145918	9US-0145919 9US-0145951	9US-0146386	9US-0146388 9US-0146389	978-0147038	9US-0147204 9'15-0147302	9US-0147302	9US-C147260 9US-0147303	9US-0147416	905-0147935 905-0147935	9US-0148171	9US-0148341	9US-0148565 9US-0148684	9US-0149368	9US-0149175 9US-0149426	9US-0149722	9US-0149723	9US-0149902	9US-0149930	9US-0150566	908-0190884 908-0151068	9US-0151066	9US-0151080 9HS-0151303	9US-0151438	
24-CUN-1999;	8-0.0N-1999 9-0.0N-1999	0-5UN-1999	1 - JUL - 1999 1 - JUL - 1999	2-JUL-1999	6-JUL-1999 8-JUL-1999	9-JUL-1999	2-00L-1999 3-JUL-1999	4-JUL-1999	5-JUL-1999 6-JUL-1999	6-JUL-1999	9-JUL-1999 9-JUL-1999	9-JUL-1999	9-00L-1999 9-JUL-1999	9-JUL-1999	0-JUL-1999	0-JUL-1999	1-JUL-1999	1-JUL-1999	2-CUL-1999 2-JUL-1999	2-JUL-1999	2-00E-1999 3-JUI-1999	3-JUL-1999	3-JUL-1999	6-00L-1999 7-JUL-1999	7-JUL-1999	/ - JUL - 1999 8 - JUL - 1999	2-AJG-1999	2-AUG-1999 2-AUG-1999	3-AUG-1999	4 - AUG - 1999 4 - AUG - 1999	5-AUG-1999	5-AUG-1999 6-AUG-1999	6-AUG-1999	9-AUG-1999 9-AUG-1999	0-AUG-1999	2-AUG-1999	3-AUG-1999 3-AUG-1999	6-AUG-1999	7-AUG-1999 8-AUG-1999	0-AUG-1999	0-AUG-1999	3-AUG-1999	3-AUG-1999	5-AUG-1999 6-AUG-1999	7-AUG-1999	7-AUG-1999	7-AUG-1999 0-AUG-1999	1-AUG-1999	
K K K	ፓ <i>ኒ</i> ' ኧ ኧ	PR :	ች 모	P. 6	ጟ ጟ	PR (ያ ር አ አ	F. C.	ያ ው አ	8 8	አ	۲. در در	ጸ <u>ዋ</u>	PR 00	7 K	P. C.	۲ ۲ ۲ ۲	۲. در د	R R	ማ ር	רי ני הי 50	(C4	g. 6	7, 2, 2, 2,	80.0	7. K	PR	7 Y	ዋ	2 2	, D.	ያ ያ	٣.	ታ <u>ዋ</u> ጙ ጙ	9. 9.0	P. P.	PR PR	ጸ		PR	8 8 9	7. X.	PR	P.R.	, K	R.	7. Q	P.R.	

```
203 YQDFILKRLENFVRELYSLGVRNVLV--GGLPPM--GCLPI-HMTAKFRNIFRFCLEHHN 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 KDSVLYNEKLQNLIPQIEASLPG-SKFLYADVYN--FMMEXIQNPSK-----YGFKETKR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TISPKVQRADSDVIPSNSPGERNVVVTBGDLKKVLDGCAPLIRFINKLRTFGRTFTBAYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 SEQPNYFKSYIARIKGIVGDKKAMEIINNAFVVVSAGPNDFILNYYEIPSRRLEYPFISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 SNISNLVITDASSLNGV--DKKLLSAEVERMLVQKGAPNEGI----EVVFGLILYALAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DECIAYKHKLPQLNAAABLGIPABDSYLAADFLGTCPKLSELQQSRKMFASMYALK-TBG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
8.7%; Score 86; DB 21; Length 366;
Best Local Similarity 26.5%; Pred. No. 1.3;
Matches 49; Conservative 23; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG39165 standard; Protein; 366 AA.
99US-0151930.
99US-0152363.
99US-0153758.
99US-0154018.
99US-0154018.
99US-0154039.
99US-0155139.
                                                                                                                                    990S - 0155659
990S - 0156458
990S - 0157855
990S - 0157855
990S - 0157865
990S - 0157865
990S - 0157865
990S - 0159231
990S - 0159231
990S - 0159331
990S - 0159638
990S - 016098
990S - 0161406
990S - 0161406
990S - 0161369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVVNT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 GCCGT 314
01. SEP 1999

10. SEP 1999

13. SEP 1999

14. SEP 1999

22. SEP 1999

23. SEP 1999

24. SEP 1999

25. SEP 1999

26. SEP 1999

27. SEP 1999

28. SEP 1999

29. SEP 1999

29. SEP 1999

20. CCT 1999

20. CCT 1999

21. CCT 1999

22. CCT 1999

23. SEP 1999

24. SEP 1999

25. CCT 1999

26. CCT 1999

27. CCT 1999

28. SEP 1999

29. CCT 1999

20. CCT 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
AAG39165
ID AAG39
XX
AC AAG39
   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

202

AAG39165;

```
9908 - 0139750 - 9908 - 0139751 - 9908 - 0139817 - 9908 - 0139817 - 9908 - 0139817 - 9908 - 0139817 - 9908 - 013981 - 9908 - 013981 - 9908 - 014082 - 9908 - 014082 - 9908 - 014082 - 9908 - 014292 - 9908 - 014292 - 9908 - 014292 - 9908 - 014292 - 9908 - 014292 - 9908 - 014292 - 9908 - 014292 - 9908 - 014292 - 9908 - 014292 - 9908 - 014292 - 9908 - 014292 - 9908 - 014292 - 9908 - 014292 - 9908 - 014292 - 9908 - 0145918 - 9908 - 0145918 - 9908 - 0145918 - 9908 - 0145918 - 9908 - 0145918 - 9908 - 0145918 - 9908 - 0145918 - 9908 - 0145918 - 9908 - 0145918 - 9908 - 014792 - 9908 - 014792 - 9908 - 014792 - 9908 - 014792 - 9908 - 014793 - 9908 - 014793 - 9908 - 014793 - 9908 - 014793 - 9908 - 014793 - 9908 - 014972 - 9908 - 014972 - 9908 - 014972 - 9908 - 014993 - 9908 - 014993 - 9908 - 014993 - 9908 - 015998 - 9908 - 015998 - 9908 - 015998 - 9908 - 015998 - 9908 - 015998 - 9908 - 015998 - 9908 - 015998 - 9908 - 015998 - 9908 - 015998 - 9908 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015998 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 - 015908 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-1999
02-AUG-1999
03-AUG-1999
04-AUG-1999
04-AUG-1999
05-AUG-1999
06-AUG-1999
06-AUG-1999
09-AUG-1999
11-AUG-1999
11-AUG-1999
13-AUG-1999
20-AUG-1999
20-AUG-1999
20-AUG-1999
20-AUG-1999
20-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-1999;
25-AUG-1999;
26-AUG-1999;
18-JUN-1999;
18-JUN-1999;
21-JUN-1999;
23-JUN-1999;
23-JUN-1999;
24-JUN-1999;
29-JUN-1999;
20-JUN-1999;
01-JUL-1999;
02-JUL-1999;
02-JUL-1999;
06-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           999999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9-JUL-1
0-JUL-1
0-JUL-1
      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 48419.
                                                                                                                                                                                                                                                                                                                                   99US - 0121825
99US - 0125788
99US - 0125788
99US - 01257862
99US - 01257862
99US - 0126785
99US - 0128714
99US - 0130077
99US - 0130077
99US - 0131489
99US - 0132486
99US - 0134886
99US - 0136782
99US - 0139458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990S-0139459.
990S-0139460.
990S-0139461.
990S-0139462.
                                                                                                                                                                                                                                                                                           25-FEB-2000; 2000EP-0301439
                    18-OCT-2000 (first entry)
                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                   25-FEB-1999,
05-MAR-1999,
23-MAR-1999,
25-MAR-1999,
29-MAR-1999,
06-APR-1999,
06-APR-1999,
19-APR-1999,
19-APR-1999,
19-APR-1999,
23-APR-1999,
23-APR-1999,
23-APR-1999,
23-APR-1999,
23-APR-1999,
23-APR-1999,
26-APR-1999,
06-MAY-1999,
06-MAY-1999,
06-MAY-1999,
06-MAY-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03 - JUN - 1999

03 - JUN - 1999

04 - ZUN - 1999

06 - ZUN - 1999

10 - ZUN - 1999

14 - ZUN - 1999

16 - JUN - 1999

16 - JUN - 1999

18 - J
                                                                                                                                                                                                                     EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MAY-1999;
-MAY-1999;
-MAY-1999;
-MAY-1999;
-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -MAY-1999;
-MAY-1999;
-MAY-1999;
-MAY-1999;
-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -MAY-1999;
-MAY-1999;
-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - JUN-1999;
8-JUN-1999;
8-JUN-1999;
8-JUN-1999;
8-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999;
1999;
1999;
                                                                                                                                                                                                                                                        C6-SEP-2000
```

```
The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilitic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 1.0 degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB899132-AAB999143,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VVTEGDLKKVidgcapltrftn-Kirtfgrtft 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S KLESFIVEKWAERK-VPGISISII-------KDGDVVYAKGFGYRNVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKVQRADSDVIFSNSFGERNV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58;
                                                                                                                                                                                                                                                                                                                                                                                                        New nucleotide sequences isolated from Pyrococcus abyssi encode
proteins useful in industry -
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.7%; Score 86; DB 22; Length 447; 26.0%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                         Lecompte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Indels
                                                                                                                                  Hyperthermophilic archaeon, hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                         Forterre P, Thierry JC, Prieur D, Dietrich J, Squerellou J, Weissenbach J, Saurin W, Heilig R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 EAYVDFCIAYKHKLPQLNAAAEL--GIPAEDSYL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---VHHLLTHSSGIPSLGYAEAFIDGMVGGDNWL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Pages 693-694; 1657pp; French.
                                                                                                                                                                                                                                                                                                 (CNRS ) CNRS CENT NAT RECH SCI. (IFRE-) IFREMER INST FR RECH EXPL MER.
                          AAB96072 standard; Protein; 447 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW17788 standard; Protein; 599 AA
                                                                                                          Putative P. abyssi beta-lactamase.
                                                                                                                                                                                                                                            99FR-0005034.
                                                                                                                                                                                                                                                                       99FR-0005034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Pest Local Similarity 26.00.
Pest Local Occervative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1997 (first entry)
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-126236/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 AA;
                                                                                                                                                                Pyrococcus abyssi
                                                                                                                                                                                                                                            21-APR-1999;
                                                                                                                                                                                                                                                                       21-APR-1999;
                                                                                                                                                                                        FR2792651-A1
                                                                               29-CCT-2001
                                                                                                                                                                                                                   27-CCT-2000.
                                                     AAB96072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW17788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
AAW17789
RESULT 12
AAB96072
                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ď.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQPNMFKSYIARLKGIVGDKKAMEIINNAFVVVSAGPNDFILNYYEIPSRRLEYPFISG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 YQDFILKRLENFVRELYSLGVRNVLV--GGLPPM--GCLPI-HMTAKFRNIFRFCLEHHN 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DECLAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCFKLSELQQSRKMFASMYALK-TEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 KOSVLYNEKLONLLPQIEASLPG-SKFLYADVYN--PMMEMIÇNPSK-----YGFKETKR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 SNLSNLVITDASSLNGV--DKKLLSAEVEKMLVQKGAPNEGI----EVVFGLLLYALAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

8.7%; Score 86; DB 21; Length 36

Best Local Similarity 26.5%; Pred. No. 1.3;

Matches 49; Conservative 23; Mismatches 93; Indels
                                                                                                      990S-0153758
990S-0154018
990S-0154018
990S-0154018
990S-0155466
990S-0155466
990S-0156458
990S-0156458
990S-0156458
990S-0156458
990S-0158029
990S-0158029
990S-0158029
990S-0158029
990S-0159034
990S-0159038
990S-0159038
990S-0159038
990S-0159038
990S-0159038
990S-0160816
990S-0160816
990S-0160816
990S-0160816
990S-0160816
990S-0160816
990S-0160816
         99US-0151C66.
99US-0151080.
99US-0151303.
99US-0151330.
99US-0151330.
99US-0153363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVVNT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                         R 21-007-15
21-007-19
21-007-19
22-007-199
22-007-199
25-007-199
25-007-1999
26-007-1999
26-007-1999
26-007-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310
                                                                                                                                                                                                                              28-OCT-1
```

g

ਨੇ

ò ਪ੍ਹ ò a ö

```
261 EFLNEFNLICRENNLIINDNKTKVDNFPFVDXSSKSDIFSFFENITSTNSNDXWIKEISN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 FIDYCVNEEHLGNKGAIKCIFPVI-----TNTLKQKKVDTKNI-DNIFSKRNMVTNFN 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- ASSINGVDK--KILSA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLRAV-5; grapevine leafroll virus, GLRAV infection, GLRAV coat protein;
GLRAV HSP70 homologue protein; viral gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVERMLVQKGAPNEG-IEVVFGLLYALAARTISPKVQRADSOVIFSNSFGERNVVVTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AbiE (AAW17788) is a phage abortive infection protein that increases resistance to phage. It is the expression product of an open reading frame found in the 4.5 % EcoRI fragment (AAT68648) of Lactococcus lactis (L.L.) subsp. lactis WI plasmid pSRC860. AbiE acts at, or before, phage replication and has no homology with known Abi proteins. It protects against phages of 936 and P335 types, also against c2 when present on a high copy number plasmid. AbiE can be used to impart phage resistance to bacteria, esp. L.I. that no not have natural resistance. The recombinant bacteria can be used in the produ. of fermented dairy products.
                                                                                                                                                                                                                                                                                                                                                                                                              Isolated DNA encoding the AbiE protein of Lactococcus - for protecting strains used in production of fermented dairy products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.6%; Score 85; DB 18; Length 599;
24.3%; Pred. No. 3.3;
Live 26; Mismatches 46; Indels
                                 AbiE; abortive phage infection protein; phage resistance; pSRQ800; lactic acid bacterium.
                                                                                                                                                                                                                                                                                                         Vandenbergh PA;
                                                                                         Lactococcus lactis subsp. lactis isolate Wl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLKKVLDGCAPLTRFTNKLRTFGRTFTE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFEKILDLSLKDSRLTNKFLTFFENINE
Phage abortive infection protein AbiE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 48; Page 30-32; 49pp; English
                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                                                                                                           Moinean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ELMSDSNL----SNLVITD--
                                                                                                                                                                                                96WO-IB01385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY97690 standard; Protein;
                                                                                                                                                                                                                                    95US-0565907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant disease resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grapevine leafroll virus
                                                                                                                                                                                                                                                                                                         Kondo JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLRaV-5 coat protein.
                                                                                                                                                                                                                                                                      (UNIT ) QUEST INT BV
                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-319765/29.
N-PSDB; AAT68648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
Les 36; Conserv
                                                                                                                                                                                                                                                                                                                        Vedamuthu ER;
                                                                                                                                                                                                20-NOV-1996;
                                                                                                                                                                                                                                    01-DEC-1995;
                                                                                                                             WO9720917-A2
                                                                                                                                                               12-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                       Holler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            े
```

9

```
This sequence represents a grapevine leafroll virus (GLRaV-5) protein sequence of the invention. The DNA sequence can be used in an expression construct. The construct is useful for providing resistance to GLRaV infection in a recombinant plant cell by transforming the plant cell with it, where transcription of the polynucleotide sequence interferes with a normal viral function such as movement, encapsidation or replication of viral RNA. The polynucleotide sequence is expressed as an antisense viral RNA. The polynucleotide sequence is expressed as an antisense cat encodes a GLRaV coat protein, preferably a defective GLRaV coat protein or a GLRaV HSP70 homologue protein. The GLRaV-5 DNA is useful for the synthesis of GLRaV, as diagnostics and probes, for viral seme mapping and for induced plant disease resistance. It Is also useful to detect and quantitate expression of GLRaV in plant tissue prior to use in vegetative propagation, by detecting the presence of GLRaV RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TISPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLIRFINKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 OGISSGKLEV-NIKICASHGVPPNYYPYSPDCLHVDARLFGYDASLAAE-LGKMVAINKP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protective polypeptide antigen; PPA; Fulisawa strain; swine erysipelas; recombinant production; immunogenic; subunit vaccine; transmucous administration.
                                                                                                                                                                                                                                                                                                       Novel grapevine leafroll virus polynucleotide useful as diagnostic and
probe, for viral gene mapping and for induced plant disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 STSPKVSSSSNRTI-TGKYDGKEVTVAHDEIKTALDNSIGSFGYENTPROFGRAFTAAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DECIAYKHKLPQLNAAAELGIPAE-------DSYLAADFLGTCPKLSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erysipelothrix rhusiopathiae protective polypeptide antigen fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 84.5; DB 22;
24.4%; Pred. No. 1.2;
tive 21; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB14800 standard; Protein; 402 AA
                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erysipelothrix rhusiopathiae
                                                                                                                                   99US-0144453.
                                                                                               19-JUL-2000; 2000WO-US19708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 24.4%
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQSRKMFASMY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNSNRATHNLY 254
                                                                                                                                                                        (AGRI-) AGRITOPE INC
                                                                                                                                                                                                                                               WPI; 2001-147339/15.
N-PSDB; AAA91259.
                                                                                                                                                                                                            Monis J;
                    WO200105957-A2
                                                                                                                                   19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP3072345-B1
                                                        25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB14800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                          Good XC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
AAB14800
qc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
```

31-JUL-2000

```
This sequence represents a 46.5 kD immunogenic fragment of the protective polypeptide antigen (PPA) of the bacterium Erysipelothrix thusiopathiae. This bacterium infects livestock, particularly pigs (swine erysipelas), and is also able to cause disease in humans. The recombinantly produced PPA fragment may be used as a subunit vaccine for shimulating an immune response in animals against Brysipelothrix rhusiopathiae. As the vaccine can be produced recombinantly, it can be produced on a large scale. The vaccine is suitable for transmucous
                                                                                                                                                                                                                                Novel recombinant protective polypeptide antigen useful as a vaccine for protecting livestock against Erysipelothrix rhusiopathiae infection
                                                                                                       (NORQ ) NORINSUSANSHO KACHIKU EISEI SHIKENJOCHC.
(HGET ) HIGETA SHOYU KK.
(FUJI-) FUZITA GAKUEN.
                                                                                                                                                                              WPI; 2000-551432/51.
N-PSDB; AAA72313, AAA72317, AAA72318.
                                                                                                                                                                                                                                                                                                        Claim 1; Page 14-15; 23pp; Japanese.
                                     99JP-0094004.
                                                                       99JP-0094004
                                     31-MAR-1999;
```

60 RTTSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFT--- 116 50; Indels 29; Gaps Query Match

8.2%; Score 81.5; DB 21; Length 402;
Best Local Similarity 24.8%; Pred. No. 4.5;
Matches 33; Conservative 21; Xismatches 50; Indels 29 ò

Sequence 402 AA; administration.

25 ç 2b ò

166 -- RKMFASMYALK 176

ELHPLYLELYAWR 239

completed: November 7, 2003, 14:48:31 ne : 42 secs Search co: Job time

On Run

```
AF114061 Grapewine
AF114061 Grapewine
AF056575 Beet yellow
AF056575 Beet yellow
X73475 Beet yellow
X73476 Beet yellow
A719476 Beet yellow
A719476 Beet yellow
A71948 Beet yellow
A71948 Citrus tr
AF198114 Citrus tr
AF14289 Citrus tr
AF14289 Citrus tr
AF14289 Citrus tr
AF14289 Citrus tr
AF184116 Citrus tr
AF22050 Citrus tr
AF342899 Citrus tr
AF342899 Citrus tr
AF342891 Citrus tr
AF342893 Citrus tris
AF342893 Citrus tr
                                                                                                                                                                                                                                                                                                                                                                                            AF039204 Grapevine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF184113 Citrus t
AF456773 Citrus t
AF501868 Citrus t
AY190048 Citrus t
                                                                                                                                                                                                                                                                                                                                                                           AR138306 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          AR138299 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           Y14131 Grapevine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF501869 Citrus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF220505 Citrus
AF339088 Citrus
                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF220534
CTR297732
                                                                                                                                                                                                                                                                                                                                                                                                                       GLAV4131
AF314061
AF190581
BYU71295
AF056575
BYUMBPA
CLBYV3PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF184115
AF342894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AY170468
CTU16304
AF184117
AF184116
AF220502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF342895
AF184118
AF342891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITV18420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF342892
AF342893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF220505
AF339088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF184113
AF456773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF501868
AY190048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF342890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTVCOATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BYU51931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF501867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF220503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF184114
                                                                                                                                                                                                                                                                                                                                                                                                          AR138299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BYVUAA
A41914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTVCOAT
                                                                                                                                                                                                                                                                                                                                                                         AR138306
                                                                                                                                                          em_htgo_hum: *
em_htgo_mus: *
em_htgo_other: *
             htg hum: *
htg inv: *
htg other: *
                                                                htg mus: *
htg pln: *
htg rod: *
                                                                                                                htg_mam:*
htg_vrt:*

        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф
        ф

                                                                                                                                                                                                                                                                                                                                           Length DB
                                                                                                                                                                                                                                                                                                                                                                           597
15500
15500
8590
16527
15468
15468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2724
5980
6746
15480
783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     672
1080
19293
19296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19226
19259
19259
                                                                                                                                                  sy:
                  Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        9991
991
991
984
921
297
293
293
286
286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266.5
130.5
129.5
125.5
125.5
125.5
125.1
125.1
                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124.5
123.5
123.5
123.5
123.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120.5
120.5
120.5
120.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120.5
120.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Command line parameters:
-MODEL=frame+_p2n.model -DEV=xih
-Q=(cgn2_1/USPTO_spool/US09613486/runat_07112003_120411_27395/app_query.fasta_1.391
-Q=(cgn2_1/USPTO_spool/US09613486/runat_07112003_120411_27395/app_query.fasta_1.391
-DB=GenEmbl -QFMT=fastap -SUFFIX=+ge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=sext -HERASIZE=2600 -MINLAR=0 -MAXEN=200000000
-USRE-US09613486 GCGN i 1 3509 @runat -0112003 120411 27095 -NCPU=6 -ICPU=3
-NO_NMAP -LARGEQÜERY -NEG-SCORES=0 -WAIT -DSPBLCK=±100 -LONGLOG
-NO_NM=20 -LARGEQÜERY -NEG-SCORES=0 -WAIT -DSPBLCK=±100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPOP=10 -YGAPOP=6 -DELEXT=7
                                                                                                         ; Search time 3510 Seconds
(without alignments)
2307.723 Million cell updates/sec
                                                                                                                                                                                                        1 MELMSDSNLSNLVITCASSL......GGVVNTPVSNLRQLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                         5777422
             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
                                                                            nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                       2888711 segs, 20454813386 residues
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                            20:29:33
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                        0.5
                                                                                                                                                                                                                                                    Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                            2003,
                                                                                                                                                                                                                                                                                                                                                                                                        length: 0
length: 2000000000
                                                                                                                                                                        US-09-613-486-15
991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gobba:

gobba:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_pat:...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_or:
                                                                                                           ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenEmbl:*
                                                                                                            November
                                                                                                                                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10:
                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                        Scoring table:
                                                                            OM protein
                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
```

AR138306 597 bp Seguence 14 from patent US 6197948.

GI:14479815

AR138306.1

Unknown Unknown.

ORGANISM

REFERENCE

AR138306

ACCESSION VERSION KEYWORDS SCURCE

LOCUS

AR138306

RESULT 2

d

423

191 481 181

5

```
Plant Pathology, Cornell University, N
Experiment Station, Geneva, NY 14456,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Grapevine leafroll-associated virus
/mol_type="genomic RNA"
/db_xref="taxon:64003"
                                                                                                                                         JNA stage;
                                                                                                                                                                                              McFerson, J.R.
                                                                                                                                           9
                                                                                                                                                                                                                                                                 closterovirus type member
č. Gen. Virol. 79 (Pt 5), 1289-1298 (1998)
98264537
                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 15000)
Zhu,H.Y., Ling.K.S. and Gonsalves,D.
Zhu,H.Y., bing.K.S. and Gonsalves,D.
Submission
Submitted (18-DEC-1997) Plant Pathology,
York State Agricultural Experiment Statio
                                                                                                Grapevine leafroll-associated virus 2
Grapevine leafroll-associated virus 2
Viruses; SSRWA postlive-strand viruses,
Closteroviridae, Closterovirus.
1 (bases 1 to 15000)
Zhu,H.Y., Ling,K.S., Goszczynski,D.E., M.
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                    GI:3123909
                                                                                                                                                                                                                                                                                                                                                                                                                                              .15000
                                                                    AF039204.1
                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                              JCURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                             TITLE
16-JUN-2901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuThrargPheThrasnLysLeuargThrPheGlyargThrPheThrGlualaTyrVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsoPheCysIleAlaTyrLysHisLysLeuProGlnLeuAsrAlaAlaAlaGluLeuGly 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleProAlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluLeuGlnGlnSerArg_vsMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGly 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluArgAsnValValValThrGluGlyAspLeuLysLysValLeuAspG.yCysAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MetGlubeuMetSerAspSerAspbeuSerAspLeuVallleThrAspAlaSerSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AsnGlyValAsplysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrThrSerProLysValGIrArgAlaAspSerAspValIlePreSerAsnSerPhGCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAATTACAGCAAAGTAGGAAGATGTTCGCGAGTATGTACGCTCTAAAAACTGAAGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValValAsnThrProValSerAsnLeuArgGlnLeuGlyArgArgGluValMet 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.

1 (bases 1 to 597)

1 (bases 1 to 100 K.-2)

1 (bases 1 to 597)

Grapevine leafroll virus (type 2) proteins and their uses Patent: US 6197948-A 14 36-WAR-2001;
PAT
```

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

1.95e-97 991.00 100.00% 100.00%

Percent Similarity: Best Local Similarity: Query Match:

DB:

Alignment Scores: Pred. No.: Score:

(1-597)

US-09-613-486-15 (1-198) x AR138306

-1

ò CP. ò 20 $\stackrel{>}{\circ}$ g ે

21

61 41 121 181

qq

; 8

ò a $\dot{\varsigma}$.g à ď ò d ò

3

101

301

121 361 141

154

165 a

source BASE CCUNT ORIGIN

AUTHORS TITLE JOURNAL FEATURES

Location/Qualifiers /organism="unknown" 121 c 157 g

```
AGLIRERAGGREPLUZZER IRPAGECYLAHCRAY, CAFLLEGEBORGEDY
AAMFSFAAGGREPLUZZER IRPAGECYLAHCRAY, CAFLLEGEBORGEDY
YAAMFSFAAGGREPLUZZER IRPAGECYLAHCRAY, CAFLLEGEBORGEDY
KLARNEWSELGERSLGZULYGGTDSGLZKLGIEKOLIDEKUJOYOSLKYDPI VROPEY
KLARNEWYSELGERSLGZULYGGTDSGLZKLGIEKOLIDEKUJOYOSLKYDPI VROPEY
PSDATTOMSLITEY POPEL KESHSSHSDH-PAAAGRILENETJURLCCNSVSDIGGESY
KSTATOMSLITEY POPEL KESHSSHSDH-PAAAGRILENETJURLCCNSVSDIGGESY
FHLHSKTORRYHYOVYDAYDORDORROWNELOLG'S NURHGDDDSKLLGGRNENDE
FHLHSKTORRYHYOVYDAYDORNORRYNEWRENDEDGSBCVYMBEZD
GETSYNOWNYKFGSSGYSHKLSIIKDIMTPYLTLGGFLESVENYSUNYSKY
KITKSBVSPISGCKLLRYRRANDOWVKYKERNCLFOGYDIIVLDGKYVNSEN
KITKSBVSPISGCKLLRYRRANDOWVKYKERNCLFOGYDIIVLDGKYVNSEN
KITKSBVSPISGCKRLENRRANDOWVKYKERNCLFOGYDIIVLDGKYVNSETAAMLAS
GVARRLASFYLAKLSHFSGDCSFIEATSFVLREKTRNHLAFBRLLGLYKRYAFAT
LDVSFILDLSSTLESITDPACKYNISJERTANTLANFBRLLGLYKRYAFAT
LDVSFILDLSSTLESITDPACKYNISJERTSFYLREKTRNHLAFBRLLGLYKRYAFAT
TOORDISKSPSRYGVORSSENDAKRREVORPGLAGGSRNOWVGFFHHYVDSALRLFKYA
TOORDISKSPSRYGVORSSENDAKREVORPGLAGGSRNOWVGFFHHYVDSALRLFKYA
TOORDISKSPSRYGVORSSENDAKREVORPGLAGGSSNOGAFLAGVYRNYRY
VTHGLSTTANDGVIRGVYSGIVSHLLVGNYGNYRYRGSSSSOGAEBFRANDERIN
TTYNOVYDAYVVRNYNYNYRYSGIVHTGRANGYRGSSSSOGAEBFRANDERIN
GGSSYGFSILAFFRIMMGARRIIVYKNYRFCKSTEFLSLKLHERFTRVGGURKTDV
GVYDFLATGIVETLSSIEEDGDIRGLEGOBSSSOGAEBFRENDFLASIEEP
PRACIRGGSSAIAILAILENTWRANDALCHNNEFYVKSFALDFNANDALGSSPLASIEEP
PRACIRGGSSAIAILAILENTWRANDALGALMNEFYVKSFALLDRALMKRANGSTERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /1. 7423
/function="replication and unknown functions"
/function="replication and unknown functions"
/note="larger than 277 kDa; ORFla; contains domains for
/note="larger than 277 kDa; ORFla; contains domains for
two papain-like leader proteases, a methyltransferase and
a helicase; identified by sequence comparison"
/codon start=2
/product="methyltransferase/helicase polyprotein"
/product="methyltransferase/helicase polyprotein"
/product="methyltransferase/helicase polyprotein"
/br kref="GI:13123910"
/translation="ADYVAMIRYVOGGKFPLVLMSRVIYPDGRCYLAHMRYLCAFYCR
PFRESDAJGMWPTVARLARAVERNGVEAGIALRGYYTSRRVYHOVDGSATVXYFR
NJGGRIGGGSFRPFILJYGNIANESCHOSSILSGLFGALLCOIRYVERVDSGGIQSS
VKTKREDAHRTVEERAAGGSVEQPRQKRIDEKGGGRVPSGGFSHLLVGNIANEVRRKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKYVSLSNFFCHLFSSDVDDSSASAGLKGGASRMTLFHLLVRLASALLSLGWEGLKLL
LSHHNLLFLCFALVDDVNVLIKVLGGLSFFVQP:FSLFAAMLLQPDRFVBYSEKLVTA
FEFFLKCSPRAPALLKGFFECVANSTVSKTVRRLLRCFVKMLKLRKGRGLRADGRGLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RQKAVPVI PSNRVVTDGVERLSVKMQSVEALRTELR I LEDLDSAVI EKLARRRNDTN
DDEFTRPAHEQMQEVTTFCSKANSAGLALERAVLVEDA I KSEKLSKTVNEMVRKGSTT
SEEVAVALSDDEAVEEI SVADERDDSPKTVR I SEYLNRLNSSFEFFRP I VVDDNKDTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGFSYMCVSAERREKFFALVCLIGLSLPFFVRIVGAKACEELVSSARRFYERIKIFLR
polyprotein gene, partial cds; and RNA-dependent RNA polymerase, publisher transmembrane small hydrosphobic protein, 65 kDa chaperone protein, 63 kDa protein, 25 kDa diverged coat protein, 22 kDa coat protein, 19 kDa protein, and 24 kDa protein genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence and genome organization of grapevine
leafroll-associated virus-2 are similar to beet yellows virus, the
```

CDS

```
13323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13143
                                                                                                                                                                                                                                                                                                            //codon_start=1
//codon_start=1
/product="22 Aba coat protein"
/product="22 Aba coat protein"
/product="23 1329]ef "
/dx xxef="ct:31239]ef "
/translation="WELMSDSNLSMLVITDASSLNGVDKKLLSAEVERALVCKGAPNE
GIEVVPGLLJYALAARTTSPKVQRADSDVIFSNSFGERNVVTTEGDLKKVLDGCAPLT
SRTNK.KRTFGRIFTDAYVDFCIAYKHLPOJNAAAELGIPAEDSYLAADFLGTCPKLS
ELQGSRRWFASWYALKTEGGVNNTPVSNLRQLGRREVM"
13680- 14165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13203
                                                                                                          /trānslation="MSSNTSVPVGGJEALETSGVVLTTRKEAVDKFFNEJKNENYSSV
DSSRLEDSBEWKEVLEKKAKESFKSELKÄTDEHVYHIIFFLIKAAKISTEREKVXVGSH
TYVVDGRYTYTVLDAAVFNMKKSLTKKYKRVMGLRAPCCACEDLYLTVAPIMSDFFFKTK
AVGMKGLPVGKEYLGADFLSGTSKLMSCHORAVSIVAAKNAVDRSAFTGGERKIVSLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="MRVIVSPYEAEDILKRSTDMLRNIDSGVLSTKECIKAFSTITRD
LACKASYOGGVDTGLYQRNOAEKELIDTVESRIKLAQDLYREKVAVHFCKDEPKELV
LAFITRKYVELIGGVGKEAVKREMRSLIKTVLNKMSLEMAFYMSPRAWKNAEWLELKFS
PVKIFRDLLLDVETLNELCAEDDVHVDKVNENGDENHILELQDSC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="WEDYEEKSESLILLRTN:NTMLLVVKSDASVELPKLICGYLRV
SGRGEVTCCNREELTRDFEGNHHTVIRSTIIOYDSESAFEEFNNSDCVVKFFLETGSV
FWFPLRSETKGRAVRHIRTFFEANNFFFGSHCGTMEYCLKQVLTETESIIDSFCEERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluArgAsnValValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13084 ATGGAGTTGATGTCCGACAGCAACCTTAGCAACCTGGTGATAACCGACGCCTCTAGTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AsnGlyValAspLysLySLeuLeuSerAlaGluValGluLySMetLeuValGlnLySG.y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13144 AATGGTGTCGACAAGAAGCTTTTATCTGCTGAAGTTGAAAAAATGTTGGTGCAGAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 AlaProAsnGluGlyIleGluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13204 GCTCCTAACGAGGGTATAGAAGTGGTGTTCGGTCTACTCCTTTACGCACTCGCGGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thr.ThrSerProLysValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCACGICTCCIAAGGITCAGCGCGCAGATICAGACGTTATATITTTCAAATAGTTTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetGluLeuMetSerAspSerAsnLeuSerAsnLeuVallleThrAspAlaSerSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14785. .15000
/note="similar to 3'UTRs of other monopartite
                                 ccat protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15000
198
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="24 kDa protein"
/protein_id="AAC40863.1"
/db_xref="G1:3123918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4253
                                    diverged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="19 kDa protein"
/protein_id="AAC40862.1"
/db_xref="GI:3123917"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Irdels:
/codon_start=1
/product="25 kDa_diverged
/protein_id="AAC40860.1"
/db_xref="Gl:3123915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-613-486-15 (1-198) x AFC39204 (1-15000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  closteroviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'codon start=1
                                                                                                                                                                                                                                                              .13680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14167. .14784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.37e-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                991.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                          /note="p22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="p24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="p19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3050 €
                                                                                                                                                                                                                                   DIGRY
                                                                                                                                                                                                                                                              3084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                              SCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        े
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                              KEVSNIECQKRKDKRSPKKSIYTIDAYLMHRGCDADVLFIDECFWHAGSYLACIEF
TRCHKVMIFGDSRQIHYIERNELDXCLYGDLDRFVDLQCRVYGNISYRCPWDVCAMLS
TYYGNIATWRGESEGKSSMRINBINSYDDLYPDVGSFTELGGSEKLBISKHFIRKG
LITKINVLTVHENQGSFGXRYMLVRLKFQBDEPFKSIRHITVALSRHTDSLTYNVLAAR
RGDATODAIQKAABLYNKFRYFPTSFGGSVIKLNVKKDVEDNSSKRASSAPLSVINDF
LNEVNPGTAVIDFGDLSADFSTGPFECGASGIVVRDISSSNITDHDKQRV
                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="RNA-dependent_RNA_polymerase"
/product="RNA-dependent_RNA_polymerase"
/protein_id="AAC40856.1"
/db_xref="G1:312391"
/translation="SVVRSQAIPRRKPSLQENLYSFEARNYNFSTCDRNTSASMFGEA_AANGCRRRCFDLDAFSSIRBDVISITRSGIEGALEKRTPSOTKALMKDVESPLEIDDEICREMACHRRCFDLDAFSSIRBDVISITRSGIEGALEKRTPSOTKALMKDVESPLEIDDEICREMACHRRCFBMTNRDFASVVSAMCHODDVYHIGEVDFSKYZKSJANAIFSPIFNEVKRIMCCLKPDINKFFFRMTNRRPFASVVSAMCHODDVYHIGEVDFSKYZKSJOAFVKAFEEDWYKKELGY
DEELLAIMMCGERLSIANTLDGGLSFTIENQRKSGASNTWIGNSLVTLGILSLYYDVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFEALYISGDDSLIFBRSE:SNYADDICTDMGFETKFMSPSVDYFCSKFVVMCGHKTF
FVPDPYKLFVKLGAVKEDVSMDFLFETFTSFKDLTSDFNDERLIQKLAELVALKYEVQ
TGNTTLALSVIHCLRSNFLSFSKLYPRVKGWQVFYTSVKKALLKSGCSLFDSFYTPFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="65 kDa chaperone protein"
/protein_id="AAC40858.1"
/db_xref="G1:3122913"
/translation="WVVFGLPGTTFSTVCVYKDGRVFSFKQNNSAYIPTYLYLFSDS
NHMTFGYEAESLMSNLKYNGGSPRDLKRWVGCDSSNLDAYLDELKFHYSVRLVX.GSC
LNETVSIGNFGGTVKSEAHLPGLIALFIKAVI9CAEGAFACTCTGVICSVPANYDSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNFTDQCVSLSGYQCVYMINEPSAALSACNSIGKKSANLAVYDFGGGTFDVSIISYR
NTFYVRASGCDLNLGGRDVDRAFLTHLFSLTSLEPDLTLDISNLKESLSKTDAEIVY
TLRGVJQRKENDYNNKNILISYMLPVYNRTLKILESTLKSYASMNESARVKCDLVLI
GGSSYLPGLADVLTKHOSVDRILKNSDPRAAVAVGCALYSSCLSGGGGLLIDCAAFT
VALARRSCHQIICARGAPIPPEGGSMDJYLARVNNSGREVAVFEGEVYKCPRKRIG
GANIRFFDIGVTGDSYAPVTFYMDFSISSVGAVSFVVRGPEGKQVSLTGTPAYNFSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSNYSWESLFKKFYGEADWKKYLSRSIAAHSSELKTLPDIRLYG
GRVVKKSBFBSALPNSFBQELGLFILSBRBVGWSKLCGITVBBAAYDLTNPKAYKFTA
BTGSPDVKGBGQKYSMEDVMNPMRLSNLDVNDKYLTBQCWSLSNSCGELINPDDKGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VALTFKDRDTADDTGAANVECRVGDYLVYAMSLÆBQRTQKSQSGNISLYEKYCEYIRT
YLGSTDLFFTAPDRIPLLTGILYDFCKEYNVFYSSYKRNVDNRFFFLANYMPLISDVF
VFQWVKPAPDVRLLFELSAAELTLEVPTLSLIDSQVVVGHILRYVESYTSDPAIDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKLEAILKSSNPRLSTAQLMVGFFCYYGEFRTAQERVVORPGVYKTPDSVGGFEINXK
DVEKFFDKLORELPNVSLRRQFNGARAHEAFKI FKNGNI SFRPTSRLNVPREFNYLNT
DYFRHANRSGLTEEEILILNNI SVDVRKLCAERACNTLPSAKRFSKNHKSNI QSSRQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="mnQVLQFECLFLLNLAVFAVTF1F1LLVFRV1KSFRQKGHEAPV
PVVRGGGFSTVV"
                           VQGKEVRLHIKDPHDPLFDGKISINKRRRGGNVLYHDNLAFLASNLFLAGYPFSRS
FVFTNSSVDILLYEAPPGGGKTTTLIDSFLKVFKKGEVSTMILTANKSSQVEILKKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALGSRSVRELHISLNNKVFLGLLLHRKADRRILFTKDEAIRYADSIDIADVLKEYKSY
GLINAVREFYYMQELALFEIHSKLCTYYDQLRIVNFDRSVAPCSEDAÇLYVRKNGSTI
                                                                                                                                                                                                                                                                                                                        cther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                              /function="replication"
/note="RGNp; 52 kDa; similar to RNA polymerases of cth
closteroviruses; presumably expressed via +1 ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9051. 10850
/nocke="p65; HSP70; similar to heat shock 70 proteins;
identified by sequence comparison"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="6 kDa, probably membrane-associated, similar t
small hydrophobic proteins of other closteroviruses"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="p63; putative heat shock protein 90 homolog"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product="putative transmembrane small hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRIKDPLVVLKOTLYEFQHKRAGWGSRSTRDLGSRADHAKGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="p25; CPd; coat protein duplicate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AASALPPJEDVELLIGKSVQKVLRGSRLEEIPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="63 kDa protein"
/protein_id="AAC40859.1"
/db_xref="GI:3123914"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAC40857.1"
/db_xref="GI:3123912"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10777. .12432
                                                                                                                                                                                                                                                        .8801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OAVMVWDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein"
                                                                                                                                                                                                                                                                  <7422.
```

SCO

CDS

27 101 LeuthrhagphethrashlysLeuargthrPheGlyArgthrPheThrClublaTytva: 120 13864 CTCACTAGGITCACTAATAACTTAGAACGTCGGTCGTCGTCGTCGTCGTCGTCGTCGTTTTCACTAGGTT 13943 27 121 AppPheCyslieAlaTytiysHistyeLeuproGlnLeuAsnalaAlaGluLeuGly 140 28 121 AppPheCyslieAlaTytiysHistyeLeuproGlnLeuAsnalaAlaGluLeuGly 140 29 121 AppPheCyslieAlaTytiysHistyeLeuproGlnLeuAsnalaAlaGluLeuGly 140 20 1401 IleProAlaGluAppSeTytLeuAlaAlaAspPheLeuGlyThrCysproLysLeuSer 160 20 14034 ATTCCAGCTGAAGTTCGTACTAAATACCCCAACTTCTGGGTACTTGCCGGGGGGGG	5 6160 76160 7	Bari, Dipartimento di Protezione delle Piante and Centro Studio virus e virosi delle colture mediterranee, via Amendola 165/A, I 70126 Bari, ITALY REMERK revised by [3] REFERENCE 3 [bases 1 to 8590] AJTHORS Abou-Gharem, N. TITJE Direct Submission JOJENAL Submitted (07-JAN-1998; N. Abou-Ghanem, Universitat degli Studi di Bari, Dipartimento di Protezione delle Piante and Centro Studio virus e virosi delle colture mediterranee, via Amendola 165/A, I 70126 Bari, ITALY COWMENT On Jan 10, 1998 this sequence version replaced gi:2369864.	1.8590
		1.44e-95 Length: 15500	

CDS

gene

CDS

```
/ noue-
/ codon start=1
/ product="hypothetical protein"
/ product="hypothetical protein"
/ protein id="CAA74568.1"
/ db_xref="G1:2369872"
/ db_xref="G1:2369872"
/ db_xref="SPTEMBL.039859"
/ translation="MRVIVSPYEAEDILKRSTDMLRNIDSGVLSTKECIKAFSTITRD
LICARAYONGVOTOCLYQRNOAEKRLIDTVESNIRLAOPLYREKNAVHECKOEPKELV
AFITRKAYVELTGVGWREAVKREMRSITKTVLNKWSLEXAFYMSPRAWKNAEWLELKFS
PVKKFROLLIDVETLINELCEDDVHYOXVNENEDENHDLELGDRC"
** cof c 2135 g 2425 t
                                                                                                                                             6949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGAGGAATGTGGTAGTAACAGAGGTGACCTTAAGAAGGTACTCGACGGGTGTGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 AsnGlyValAspLysLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGGTGTCGACAAGAAGCTTTTATCTGCTGAAGTTGTAAAAATGTTGGTGGTGCAGAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 AlaProAsnSluGly1leGluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accadencerceraserneaecececaearreaeaecerrararrereaarracreeea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G.uArgAsnValValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCACTAGGTTCACTAATAAACTTAGAACGTTCGGTCGTACTTTCACTGAGGCTTACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACTTTGTATCGCGTATAAGCACAAATTACCCCAACTCAACGCCGCGGCGGAATTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 IleProAlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTCCAGCTGAAGATTCGTACTTAGCTGCAGATTTTCTGGGTACTTGCCCGAAGCTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATTACAGCAAAGTAGGAAAATGTTCGCGAGTATGTACGCTCTAAAAACTGAAGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetGluieuMetSerAspSerAsnLeuSerAsnLeuValIleThrAspAlaSerSerieu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTCCTAACGAGGGTATAGAAGTGGTGTTCGGTCTACTCCTTTACGCACTCGCGGCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AspPheCyslleAlaTyrLysHisLysLeuProGinLeuAsnAlaAlaAlaGluLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluLeuGlnGlnSerArgiysMetPheAlaSerMetTyrAlaLeuiysThrGluGiyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 LeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValValAsrThrProValSerAsnLeuArgGlnLeuGlyArgArgGluValMet 198
           ELQQSRKYFASYYALKTEGGVVNTPVSNLRQLGRREVM'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8590
1197
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-613-486-15 (1-198) x GLAV4131 (1-8590)
                                                                                                                   codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.736-95
984.00
99.49%
99.199%
                                            7306. .7791
/note="ORF7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="CRF8"
                                                                                                                                                                                                                                                                                                                                                                                                                                         7793. .8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2344 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  707C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCUNT
                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE CC
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    े
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   검
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Trains at 10n included the Very Cead when the Very Crains and the Very Crains at 10n included the Very Crains and Very Crain
                                                                                                                                                                           /product="hypothetical protein"
/protein id="CRA74562.1"
/db_xref="CI:2369866"
/db_xref="SPTREMBL:039863"
/tb_xref="SPTREMBL:039853"
/translation="XNQVLQFECLFLINLAVFAVTFIFILLVFRVIKSFRCKGHEAPV
PVVRGGFSTVV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MVVFGLDFGTTFSTVCVYKDGRVFSFKQNNSAYIPTYLYLFSDS NHMTFGYEABSLMSNLKVKGSFYRDLKRWVGCDSNLDAYLDRLKPHYSVRLVKIGSG INTATVSIGHTSGYKSEPAHPGLIALFRAVISCAEGAFACTGGYCSVPANYDSVQ RNFTDQCVSLGGYQVYXINBPSAAALSAGNGVKKRANLAYVDFGGGFFDVSIISYR NNTFVVRASGGDLNLGGRDVDRAFLTHLFSLTSLEPDLTLVYSNLKESLSKTDARIYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TERGVDGRKEDVRVNKNILITSVMLPIVKRTLKILESTIKSYAKSKNESALVKCDLVIL
OGSSYLPGLADVLTKHOSVDRILRVSDPRAAVAVGCALYSSCLSGSGGLLLIDCAAHT
VALADRSCHQIICAPACARIPRSGSMPLYLARVNKNSQREIAVFEGEYTKCPKNRKIC
GANIRREJOUTGORY SAPVTFMPSISSVGAVSFVVRQPEGKQVSLTGTPAYNFSSV
ALGSRSVRELH SLNNKVFLGELLRRADRRILFTKDEAIRYADSIDIADVLKEYKSY
AASALPPDEDVELLLGKSVQKVLRGSRLEEIPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon start=1
/prduct=="coat protein"
/protein:id="Cat174565.1"
/db_xref="G1:2369869"
/db_xref="SPTREYBL:039856"
/db_xref="SPTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="melmsdonlsnlv1tdassingvdkkllsaevykylvokgapne
GIEVVFGLLLYALAARTTSPKVQRADSDV1FSNSFGERNVVTEGDLKKVLDGCAPLT
RFTNKLRTFGRTFTEAYVDFCIAYNHKLPQLNAAAELG1PAEDSYLAADFLGTCPKLS
DERLIQKJAELVALKYEVQTGNTTLALSVIHCLRSNFLSFSKLYPRVKGWOVFYTSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVGMKGLPVGKEYLGADFLSGTSKLMSDHDRAVSIVAAKNAVDRSAFTGGERKIVSLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRIKDPLVVLKDTLYEFQHKRAGWGSRSTRDLGSRADHAKGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=:
/product="heat shock protein 70-like"
/protuctid="CAA74563.1"
/db_xref="GI:2369867"
/db_xref="SPTREMBL:0399854"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="heat shock protein 90-like"
/protein id="CAAA764.1"
db_xref="G1:236986"
/db_xref="SPTREMBL:0399S5"
                                     KALLKSGCSLFDSFMTPFGQAVMVWDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="CAA74566.1"
|db_xref="GI;2369870"
|db_xref="SPTREMBL:039857"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=:
/product="coat_protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4403. .6058
/gene="hsp90"
4403. .6058
/gene="hsp90"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               duplicate gene"
                                                                                                                                                                                                                                                                                                                                                                                         2677. .4476
/gene="hsp70"
2677. .4476
/gene="hsp70"
                                                                                                                                          /codon start=1
                                                                          2491. .2661
/note="ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="ORF6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5970. .6641
/note="ORF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLGRY"
```

gene

CDS

CDS

CDS

NCITINIFE

ACCESSION

VERSION KEYWORDS

RESULT 5 AF314061 LOCUS

22

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE

```
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVISGVVHEVLNKIREGVLRPRVGGDMRFSRPFSSTHGCKIVANVRTNTSVMLNCTKV
NGEKFSVAIPCSVDYVAMLRYVSGGKPPLVLNSRECYPDGLCYMAHMRYLGAFPCQPF
RESDYPLGSWPSVARLKALVLKRFGDEALNIGVRGYYVSRRAFHCDYDSKYARSLARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGYVGGDEVIHSTLASTVVLKPGERARDRPKSISFGSFCCELRYVESVNPDAPRLRSE
KVLRKVEPRNGVRTESADVGSNVTRKRDARIDRKFSHLLAGSVNKVKKRIAAGVLRYR
VGGDMDFHNSFLTQAGYHLLVRRKTSSSVCVELSTPDGRLLRRDVIPCSRDYAAMLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGRPJJUMTRÖKYKNGYCYLAHCRYASAFLLKGFHPAVFDIGANPTAAKLESRWV
SVLGDRSJSLNLYGSFTSRGJFHCDYDAAYVKDLRFWSAIVAGKEBMGEVVASDIJPA
MKQKTIEAVYORLYGSNDSLLKLSIEKDJIDFKNDVQSLKKDRPVIRVFFYMSEVTQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLTRFYPOFELKFSHSTHSDHPAAAASRLLENFTLVRLCSHSVSDIGGGFLFHLNSKT
STRYHVCRPYDGAAQRYKRELQYSSVRSODBOBKILDGBSNUDVGTYFLGVCEHES
STRMMVOVYDASLYELCSAMIKKRARITYTMYTPGFFLDGBSCVYMSSLDCDIEUD
HADVVMYKFGSSCYSHKLSIIKDIMTTPYLVLGGFLFSVEMYEIRMGVNFKIIKGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPNISCSKLLRYRRANSDVVKVKLPRFDKKRRMCLPGYJIILJSKFVSRVFDYVVCN
CSAVNSKTFBWVWSFIKSSKSRVIISGKIIHKDVNLDLKYVESFAAVMLASGVRSRLA
SEYLAKVLSHFSGDCSFIEATSFVLREEIRNMTLNFNECLLGLVKRVAFATLDVSFLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSILFFFSRLVRRATIJIGRIKHRCFSKIFESISLKIHELRTFLLGKKRSDVGVYFFL
SEDVADALSSIEECDEIENLIGDGFRDMADDSLTDYMYFDFSDFLASVNGLFCAGLR
GGGRRVGMLAILNYVYNSLSIMARAASKNSTFTSLIIFSRGLVDRIRNIFSNKESVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSSLAISALPSAVAQLSFGQPAA"VAKSFYMTSLPSLGTGFTGG
ESSLPIGFGGFRIKTFSFSSYREIALFSELSIGFGGFGFRIGGBFBEFVSF
OCGPLSVCLGGWAST FAVLN:SFPFLDVASLAMDGDVYTPTKVRISKAAKKLKRAF
SIARAAARIRRSKVGNKEVRISHVQPLPAGGLRFSQNKNGTELIIIGRDVGVVARVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAPVVRRRGGGGRVPLIPLVAVSPFGVRYRCYAPSCGAIACFKNKLASRVAANDSRAE
KLLSARRRKLQQQNFNSRVAKKARDVTASRVDYAEGEVTPPRHIFFGSFSEPFPIPSS
SGMARSVLREEPAIVTCGASAPAIKETPRVSVKKADFSPAAPVPREALTPRVAKRGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDATMESITDFAECKVAVDLEELGCLRANAENEKIRNLAGDSMAAKLASEIVVDIEAK
PVAKHAEHPKSEVSEKKEHAKPGLRGGSKAGVLKEFLDFVLSSASRLFSCVADQQRIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSYLPIELLSSAICGAIVTLFSSGTSVSLNAFLLQITKSFSLELIVRNVVRVTHSLST
TATDGVMRSVFSQIISHLVGNTGNLAYQIAFLTGVVPLLVKKCVGLIFSMSEDTYSG
                                                                                                                                                                                                 VRL 06-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYVHYLDTAVSFLDQNYENLSFIMRVLSKGYSCMFSYLANRGSLANRVASAVQIVREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVLCANVSVSKAKVVVTFSAAVCAMMFNSCGFSGDGREYKSYMHRYTQVLFDT1FFED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIKHGVSEFSFITNILKYLRGQLVDELKAVVQGVFDSNKHLFRDVTQEAIRSTVMQIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAVVDGLKCAASKVYSGIVGKKTNVGEEKSRGGDDHEEYFSCDESETPGLRGGSRSG
                                                                                                                                                                 AF314061
Grapevine rootstock stem lesion associated virus
methyltransferase/helicase polyprotein, RNA-dependent RNA
polymerase, p6, HSP70-like protein, ESP90-like protein, coat
protein duplicate, coat protein, p19, and p24 genes, complete cds.
AF314061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-CCT-2000) Plant Pathology, University of California, One Shields Ave., Davis, CA 95616, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          grapevine rootstock stem lesion associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     forganism="Grapevine rootstock stem lesion associated
product="methyltransferase/helicase polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grapevine rootstock stem lesion associated virus Grapevine rootstock stem lesion associated virus Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviriaes; Closterovirus. I bases 1 to 16527)
Zhang, Y. and Rowiani, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein_id="AAN63466.1"
db_xref="GI:24636915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mol_type="genomic RNA"
db_xref="taxon:167634"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07. .8902
note="327 kDa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 16527)
Zhang,Y. and Rowhani,A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                               AF314061.1 GI:24636914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .16527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus
Unpublished
```

source

FEATURES

CDS

REFERENCE AUTHORS TITLE

JOURNAL

COURNAL

ENFTDOUGH TO THE TOTAL THE CLSAERREKFFALVCLVTLGFPYFARFLGGVVCDKLLSSLRRAYDRVIVFLKERCDÄA MNGLRCLFHFDGNGDSTSAGLKGGGSQTFLWGLLLRLVRFALSLGYAGCKCVFSHHDL FFLCVSLVBEVNMIAKILGCLSFFSRRISSALAFALLQPERFVEXSGKLSTTFLFPLK ISPVPLKIKGFFFWVAGSPELLRGVFFLALIAVKLNLERKRGLRTANGGYFSGFAVP VIPSNRVTNGGCERJSEKMGVFBALBSELRIJLELDAAVVEKINKRRREADTSBFFSR PMHESTHDVTSFCSKANSVGTALBRAVLVSDAVKSEKISRKAKDLVRKGTVSDEFITN TLSDDEA! EEVPVSEERDDSPKTVRVSEYLNRLNSSPEFPKPI VVJDNKETGGLTNAV REFYYMQELALFEI HSKLCAYYDQLR I VNFERSMAPCNEDAQLYVRKNGST I VQCKDV RSNI KDFHDHDFLFDGKI SVNRRRRSGNVLYHDNLSFLASNLFLAGYPFSRSFVFTNS SVDILLYEAPPGGGKTTTLIDSFLKVFKKGEVSTMILTANKSSQVEILKKVEKDISNI ECQKRKDKRTPKKSIYTIDAYLMHHRGCDADILFIDECFMVHAGSVLACIEFTRCHKV MIFGDSRQIHYIERNELDKCLYGDLDFFVDLQCRVYGNVSYRCPWDVCAMLSVVYDNM IATVKGEŠECKSSKRINEINSVODEJVEDMGSTYLCMLOSEKLEISKHFIRKGLSKLNV LTVHEAQGETYARVNLVRLKFQEDEPFKSIRHITVALSRHTDSLTYNVLAARRGDATC DAIQKANELVNKFRVFPTSFGGSVINLDVKKDVEDNSRCKASSAPLSVINDFLSDVNP /protein_id="AaN63467.1"
/db_xref="G1:24636916"
/db_xref="G1:24636916"
/db_xrefp="G1:24636916"
/db_xre NIKFFTEMTURDFASVVSNMLGDDDVYHIGEVDFSKYDKSQDAFVKSFEBVYYKELGV DEELLAIMMCGERLSIANTLDGQLSTIENQRKSGASNTWIGNSLVTLGILSLYYDVR HFBALYVGGDDSLIFSRKISNYADSICLADGGFETKFWSRSVYFCSKFVYMCGHYTF FYDPYKLFYKLGYVKBOKSOMPFLETFTSFKDLTSFFNDEXVIQKLAELVALKXYVO SGNTALALSVIHCLRSPSKLYPRVKGWQVFYTSVKKALFKSGCSLYESYVTPFG /tränslation="WVVFGidFGTTFSTVCVYKDGKVYSFKONNSAYIPTYLYLFSET NHMVFGYEAESLMHNAKVRGSFFRDLKRMVGCDSSNFSDYFDRLKPHYAVRPYKIGTG LNDTVIIGNYGGTVRSEVHLPGLIASFIKAMVSCAENAFSCTCTGVICSVPANYDSVQ GRTVKKSEFESATPRSFEQELGLLMLSERDVGWCKMCGITVEEAMYQITNPEAYPITA EKCDPDVKTEGQKYTMEDVMNFMRRSNLDINDKILAEQCWSLSNSCGVLINPDDKERF VALTFKANELVÄDSSNANIDCR VGDYL VYAMSLFNCR ŠÇKSQAGNI SLYEKYCAYIRT YLENTDLYFTSPDRI PLLTGILYDFCKEYNI FYSTYKRNVDNFRF FLTNYMPLISDIF VRQWYKRATDVRLLPDI SAAELTLEVPTLSLVDSQVYIGHVLRFVESYTADPALDALE EKLDAIMKKSNPHLSTANGAPETTAQRRVVQRPCYYKTPNSVGFFINMK NVEBFPDKIQREVPNYSLR QFNGARAHEAFKVFKKONI SFR PISKLMI PREPWYLNY DYFRHANRSGLSEBEVLI LINNI SVDVRKLCAFRAGSTLLPSAKRFSKGHKSSVPSLRQE /protein_id="AAN63468.i" /db_xref="G1:24636917" /trānslation="MDQVLQFECLYLLNQAVFAITFVFILLIIRVIKSFRRNVHETPI SAVRGÇGFSTVV" translation="mSNHSWGSLFKKYYGEADWRKYLSKSIVAHTANIKTLPDVQLYG" JVRKYVKNFIKSRMRGLGLRNEHVVNSFGELVPLLLRNKLSETFIYRAVPMSKWCWKV -8901. 10280
/note="53 KDs; translated via ribosomal frameshift"
/codon start=1
/product="RNA-dependent_RNA polymerase" GTTVIDFGDLSADFSTGPFECGASGIVVRDNISSSNITDHDKQRV" /product="HSP90-like protein" /protein_id="AAN63470.1" /db_xref="G1:24636919" /produčt="HSP7C-like protein" /protein_id="AAN63469.1" /db_xref="G1:24636918" KNYRDPLIALRNSLYEFRHGNRGRRV" codon_start=1 /note="65 kDa" 'note="62 kDa" ′codon start=1 .0373. .10543 12278. .13882 product="pe" 'note="6 kDa" HAVMVWDDE" .0552

140

15143

15083

160

```
join(108. 7997,7999. 9381)
/note="The polyprotein encompasses domains for papain-like leader proteinase, putative methyltrensferse, RNA helicase and RNA-dependent RNA polymerase (RARp); ORFla/b; papain-like leader proteinase is capable of autoproteolytic release from the rest of the polyprotein, and is a replicational enhancer. RRRp is presumably expressed via a + 1 ribosomal frameshift"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAF14300.1"
/db_xref="G1:6492368"
/translat_ion="WAFLNYSAVPSCAFAPAFAPHAGASPIVPDSFPCVPRYSDDISH
FRLTLSLDFSVPRPETELNARVHLERASTDNPLPSLEPLGFFAETFVLELNGSSAPFSIPS
RHIDFVVNRPFSVFPTEVLSVSSERTPSRLFALLCDFFLYCSKPGPCVEIASPSTPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLVSNCVAQIPTHAEMESIRFPTKTLPAGRILLOFHKRKYTKRPETLIIHESGLALKTS
ALGYTSKRWASRPITVKSASGRKYEAVESRKREKSRRRQKYTKRAVISAVE
PFFFEEPKGLAKKRKASLPTKGEFITFGTLRFPLSFPKEEPRLFKREVETBVKAVE
HAVPAVVSKPVRTFRPVATTGAEYVMARTQCSRRPRNHILLRSASYTFGFKKMDLOKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRL 04-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKEKKDYYVKRSKVVSSCSVTKSPLEALTSILKNLPRYSYNSERLKFYDHFIGDDFEI
                                                                                                                                                                                                                                                                                    161 GlubeuGlnGlnSerArgiysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGly 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Beet yellows virus"
/mol_type="genomic RNA"
/etrain="ByV-4"
/db_xref="taxon:12161"
/note="Californian strain; RNA transcript derived from this cDNA clone causes formation of red necrotic lesions in Claytonia perfoliata and systemic infection in Nicotiana benthamiana.
//ore.1086. 7997,7999. 9381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beet yellows virus

Viruses; saRNA positive-strand viruses, no DNA stage;

Closteroviridae; Closterovirus.

1 (bases 1 to 15468)

Peremyslov,V.V., Hagiwara,Y. and Doila,V.V.

HSP70 homolog functions in cell-to-cell movement of a plant virus

Proc. Natl. Acad. Sci. U.S.A. 96 (26), 14771-14776 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 15468)
Peremyslov,V.V., Hagiwara,Y., Alzhanova,D. and Dolja,V.V.
Direct Submission
Submitted (27-SEP-1999) Botany and Plant Pathology, Oregon State University, 2082 Cordley Hall, Corvallis, OR 97331, USA Location/Qualifiers
                                                    14984 CITAATAGAITCACTAACAAGCIGCGAACTITCGGCCGCACGITTACGGGGGGTAIGIT
                                                                                                                                                                                                  141 :lePrcAlaGluAspSerTyrLeuAlaAlaAspPheLeuGly:hrCysProLysLeuSer
                                                                                                                                                                                                                                                                                                                      15084 GAATTACAACAAAGTAGAAAAIGTTTGCAAGTATGTACGCTTTGAAGACTGAGGGGGG
                                                                                                                  AspPheCyslieAlaTyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGly
                                                                                                                                                                                                                                           15024 ATACCAGCAGAAGATTCGTACCTAGCTGCGGACTTTTTAGGTGCTTGCCCGAAACTCTCT
                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beet yellows virus strain BYV-4, complete genome AF190581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15468 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="p348"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF190581.1 GI:6492367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10611288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF190581
                                                                                                                  121
                             101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCITINISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
AF190581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roces
                                                                                                                                                  ದ್ದ
                                                                                                                                                                                                                                  ΩΩ
                                                                                                                                                                                                                                                                                                                      Ω.
                                                                                                                                                                                                                                                                                                                                                                                                                .C.
                                                           D.
                                                                                                             \delta
                                                                                                                                                                                         े
                                                                                                                                                                                                                                                                                      \delta
                                                                                                                                                                                                                                                                                                                                                                  \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="Ank63471.1"
/db_xref="G1:24636920"
/translation="MSSGTGIAVGGSEAIETSGFVLSTRKEAVDKFNELRNENYSSY
/translation="MSSGTGIAVGGSEAIETSGFVLSTRKEAVDKFNELRNENYSSY
SSRLSDQEVKEVLEKSKESFRESELASTDEHFVYHIIFLIRSAIITTSDKVKYVGSY
XYVVEGKTYVQDVNVNMIKGLTKQYKRYVJLRYAPAMGEFKTK
AIGWKGLPVGKEYLGADFLSGTSKLMSDHDRAAVSIVAAKNAVDRSAFTGGGERKIVSLY
                                                                                                                                                                                                                                                                                                                    /procedure id="MAM63472.1"
/db xxef="G1:24636921"
/db xxef="G1:24636921"
/translation="MBLMSDNLSGLVITDASSINGVDKKLLSAEVIKMLVQKGAPSC
GIETVFGLLSYALAARTYSPKYQRASSDIIFQKTYGOKTVVTTGGDLKKVLEGCAPLN
RPTNKLMFTGRTFTEAYVDFCVAYKHKMPQLNAAABLGIPABDSYLAADFLGACPKLS
BLOGSRXMFAGNYAALKTEGGVVNTPVSNLRQLGRREVX"
15200. .15665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14724 GCGCCCAGCCAAGGTATTGAAACAGTCTTTGGGCTACTGCTCTACGCTCTCGCAGCGAGA 14783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14784 ACCACATCGCCCAAAGTTCAGAGGGCTGATTCTGATATCTTTTCAAAACACTTACGGT 14843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mkvlvspyeaediltrstemlrndsgaldtrecikafstltrd
LHCAKASYQWCVDTGLCQRDCAEKRLIDTVESNLRLAHPLIREKVATHFCKDEPKELV
AFITRKYVKLTGVAAREAVKIEMRTLSKTVLNKLSLEMAFYMSPRAMKNAEWLDLRYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnGlyValAspLysLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetGluLeuMetSerAspSerAsnLeuSerAsnLeuValIleThrAspAlaSerSerLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaProAsnGluGlyIleGluValValPheGlyLeuLeuTeuTyrAlaLeuAlaAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14664 AATGGTGTCGATAAGAAACTGCTGTCTGCGGAGGTCATAAAAAATGCTTGTGCAGAAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLKIYRDLLLDVDTLNALCEEDEIHVVVTNKDEDENHDLELQEDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16527
180
10
8
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                    protein duplicate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4624 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAN63474.1"
/db_xref="GI:24636923"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1-16527)
                                                                                                                                                                                                                                                                                      /codon_start=1
/product="coat protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4224 g
                                                                      product="coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-613-486-15 (1-198) x AF314061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
product="p19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=:
/product="p24"
                         'note="25 kDa"
                                                ccdon start=1
                                                                                                                                                                                                                                                                  note="22 kDa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="19 kDa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="24 kDa'
                                                                                                                                                                                                                                             14604. .15200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5687. .16304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.26e-88
921.00
95.96%
90.91%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3429 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ಹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
CDS
                                                                                                                                                                                                                                           CDS
```

ò q g

ò g ò

ò

a

```
LLDLATKISIEVLLKQISPVDSTASSALVRRVLSEILSNFRTMGERGIFTKVFLLLGGF
SLPVFRKKVALCVPGDMATTARELEGGRSVNSIKTMCCVAAGLVDSIVD
SLPVFRKKVALCVPGDMATTARELEGGRSVNSIKTMCVCVAAGLVDSIVD
SLVSLSGVAKERVLDSFKXIIKNFLNVFRKAKVVTRTSSSTDLSEDEYFSCLESKPG
LRGGSSRFTLSRLLDIFFNFLKSSKLVIENACFSAYERIERNMKLYFFPLNSSEERA
RTIFCAGGFTVLSDSAFDEDBULRQFREQYYSSDESVTYGRFTVLBSYLNVSSREI
STENGGREPVEVANFRALVSRLLRVLPWNCRNLSDSPGLKGGNEKALLAKFIKTCV
ITACECVSQICCLRLIRLGWGTPACGLVRLFYITYSGTRVLSRVVAAAAVCFLLVRNB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDGLSDGLTMMGVSVPRRLFVALRRALSAYSNSALRRKYFEFFRGVTHHPPDVAVUET
NEVAPEPLSPEVDIDVDCDFGSDSESVSSDEVASIPRPGLHGGSRRSSNFLTSLVKVV
FKLAGRIPPELSFLFRLFRFASTRAKREKTFIGLARLFDNFSLTSVYLLQBYDS
VLNAFIDVELLLFRLRFVAYFVERRLASKREKTFIGLARLFDNFSLTSVYTLQBYDS
VLNAFIDVELCHTSRVYDLPLVSFWRGSTTKLAEVIVGSGPASFLGRMCCRVSDAG
SSSSNAGCNFXSPVFTSKFVPPPSSSGSTASMYERLEALESDIREHTJSTCRVGSDEE
EERPKEVTEPGIEHTSEDVVPIRSHSQPLSGGECSYSEDREENERANLLPHVSKIVSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRGL ETARRNKRTLRGVSEFLNA INTSNEOPRP I I VDHSPESRALTNSVREFYY JOEL
ALFELSCKLREYYDQLKVANFNROECLCDKDEDMFVLRAGQGIVVSGRNSRLPLKHFKG
HEFCFRSGGLVPYDGTSRVDTI FHTQTNFVSANALLSGYLSYRTFTFTNLSANVILYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPGGGKTTTLIKVFCETFSKVNSLILTANKSSREEILAKVNRIVLDEGDTPLGTRER
ILIDISYLANDRGLTCKVLYDECFWYHAGAAVACIEFTKOSAILEGDSRQIFYIDR
NELDTAVLSDLNRFYDESRYVGEVSKPWOVAMLSTFYPKTVATTNUVSAGOSM
QVREIESVDDVEYSSEFVYLTMLQSEKKDLKSFGKRSSVEKFTVLTVHEAGGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKVMLVRTKFQEDDPFRSENHITVALSRHVESSTTYSVJSSKRDDAIAQAIVKAXQLVD
AYRVYPTSFGGSTLDISVNPSTSDRSKCKASSAPYBVINSFLESVVPGTTSVDFGDVS
EEMGTQVFESGADNVVIRDSAPVNKSTDHDPQRVSSIRSQAIPKRKFSLQENLYSYES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEVAFGYDÄEVLSNDPSVRGGFYRDLKRWIGCDEENYGDYLEK.KPHYKTELLKYASS
KSKYRLDCYSGTVPQNATLPGLIATFVKALISTASBARCQTGVJCSVSPANYNCLQ
RSFTESCYNLSGY POVYMVNESPAALSAGCSIKGASPVLVYDFGGGTFDVSVISAL
NVTFVVRASGGDMNLGSRDIDKAFVEHLYKKAQLPVNYKIJISFLKESLSKKVSFLNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUVSEQNVKVDVLVNVSELAEVAAPFVERTIKIVKEVYEKYRGSMRLEFSVKAKLLMV
GGSSYLPGLLSRLSSYPFVEECLVLPDARAAVAGGCALYSACLRNDSFWLLVDCAAHN
LSSSSKYCESIVCVPAGSST PFTGVRYNMAGSNASAVYSAALFEGDFVKCRLNKRIF
SGDVALGDVGVFGSNTRYPLTLEINVSSVGTITFSLVGPTGVKLVGGNAAVDFSSY
QLGERVVADLHKHNSDXVKLHALTYKPFQRKKLTDSDKALFKRLSADYRREAGKFS
SYDDAVLNSSELLLGRVIPKIIRGSRVEKLD"
                                   ARGLVENLSREQLVEAQARVSVCPHTLGNCNVKSDVLIYVQVYDASLNETASAYVLKE
SKVAYLTMYTPGELLDEREAFAIDALGCOVVVDTRRDMVQYKFGSSCYCHKLSN1KN1
MLTPAFTFSGNLFSVEMYENRMGVNYYKITRSAYSPEIRGVKTLRYRRACTEVVQVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNYNFTVCERFSGPOEFGQAMAMYMLERSFDJEKVAKVRSDVIA I TEKGVRTYMSKRE
PSQLRALSSJLOKPLNEEEI ITFKLMVKRJAKVKLJSSCLVKHPPAQVI MFHRKAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIFSPCFDEFKNRVITCTNSNIVFFTEMTNSTLASIAKEMLGSEHVYNVGEIDFSKFD
KSQDAFIKSFERTLYSAFGFDEDLLDVRMQGEYTSNATTLDGQLSFSVDNQRKSGASN
AGSRLLENETLASMAKSSFSDIGGCPLFHIKRGSTDYHVCRPIYDMKDAQRRVSRELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWIGNSIVTLGILSMFYYTNRFKALFVSGDDSLIFSESPIRNSADAMCTELGFETKFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPSVPYFCSKFFWMTGHDVFFVPDPYKLLVKLGASKDEVDSEFLFEVFTSFRDLTFUL
VDERVIELLIHLVHSKYGYESGDTYAALCAIHCIRSNFSSFKKLYPKVKGWVFYGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MDCVLRSYLLLAFGFLICLFLFCLVVFIWFVYKQILFRNTPPSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MVVFGLDFGTTFSSVCAYVGEELYLFKQRDSAYIPTFVFLHSD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="HSP70 protein homolog; CRF3; required for cell-to-cell movement"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9445. .9609
note="small hydrophobic protein; ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFVLRKFANCFREKFDJAFGEAYFLTYDET'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAF14301.1"
/db_xref="G1:6492369"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAF14302.1"
/db_xref="GI:6492370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="HSP73h"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="p6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11311. .12972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .11405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARFNRSTVV
```

```
FRESNGEVLSRKAPFDESTGESFYREFSLLLFPWTYEVCKLGGVAMEOALSGMNRLSD
YNVSELNVVDVKTVGCKFNIQTVTEFVRKLNGNLAEPSLVEHCWSLSNSGGELINPKD
TKRFVSLIFKGKDVVESTDEAVVSSSYLDYLSHCLNLYETCNLSSNSGKKALYDEFLK
                                                                                                      YVIVYLETSDLEYRSLSDNPLVAGVLYDMCFEYNTLKSTYLKNIESTSCFLSLYLPLL
SELFSMYWEOPAPDVRLLFELDTTELLLKIPTINTHDSTFLYKNKLRYLESYFEDDSN
ELKVKUDSLLTRDNPELKLAQRWVGFHCYYOYRTRAQTRKVKRDAEYKLPPALGSET
INMSGVPEFDELQKKMPSVSVRRRFCGSLSHBAFSIFKRFGVGFPFITRLNVPVKYS
YLNVDYYRHVKRAGTUDDELTILSNIEFDVABNCCEREVALOARRAQFRGEKFFGWKX
VKNEVSPHARSSIRVKKSNESLLNVLMKDVGARRQGRLNPLHRKH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHDLELNVUKKGKI ESSY I DFKŠCMTRLKPSSVSYTRVSSGKPSEDFSSSYSGKTFDS
KILNRKVTFTFESGI QLVFGMYGRDQRCVSSEYLMFENVFVGAHCGTLPYCLNCELDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAP14307.1"
/db_xref="G1:6492375"
/tb_xref="G1:6492375"
/tb_msl="Lon="MRFFPNDCETSRAISRSESLIRRVKELGTNSPQSEVSECINEFN
ELARFYHLLVTVEHERMEKHPRQSSELRTPSRLGEMLKEIRAFLKVRVVTPWHKETA
SETLNAFLEEYCRITGLIREDALREROMRKVRSTVLFHHSELLKFEVTENMFSFTELLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'translation="MTSSVELAQTKPLFRVLLLKGFVFYIVAIETEEESPEVELPLVY
                                    translation="MTTRFSTPANYYWGELFRRFFGGREWKNLMSEAASVRRPVTDRD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 SerAsnLeuSerAsnLeuValIleThrAspAlaSerSerLeuAsnGlyValAspLysLys 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="enhancer of RNA accumulation"
/note="21 kDa protein; ORF8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15468
71
32
84
2
2
                                                                                                                                                                                                                                                                           product="minor capsid protein"
protein id="AAF14304.1"
db xref="G1:6492372"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="20 kDa protein; ORF7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4434 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein_id="AAF14306.1"
db_xref="GI:6492374"
/protein_id="AAF14303.1"
/db_xref="GI:6492371"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-613-486-15 (1-198) x AF190581 (1-15468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENLSLRVISSQILGIAV"
                                                                                                                                                                                                                       12920. .13570
/note="ORF5; CPm"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGGELEILTFSKNEVFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      produčt="p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297.00
54.50%
37.57%
29.97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3471 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3866 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
CRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                         SCO
                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

CDS

SOS

```
VRL 02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArglysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrPro 185
                                                                                                                                                                                                                         AsniysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCyslleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 AACAAATTGCGGTGTTTCTGCGCACTTTCAGAAGGATTACATATCCTTCGCGAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyriysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACCGAGGAAGACTGCCTCCGATTGCTAGAGCCAACCGTCACGGTCTACCTGCTGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 SerTyrLeuAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTACTTAGCTGCTGATTTCATATCGACATCAACAGAACTTACCGACCTACAACAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peremyslov,V.V., Hagiwara,Y. and Dolja,V.V. Genes required for replication of the 15.5-kilobase RNA genome
                                                                                                                                                                                                    SerAsmieuSerAsmLeuVallleThrAspAlaSerSerLeuAsmGlyValAspiysLys
                                                                                                                                                                                                                                                                        27 LeuleuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                      GlnArgAlaAspSerAspValllePheSerAsnSerPheGlyGlu---ArgAsnValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                         ValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaProLeuThrArgPheThr
                                                                                                                                                                                                                                                                                                    91 AAACTACGGAGGAATTTCGAAGAGTGTTTGAAATTGAAAGGGGTTCCGGAAGATAAACTC
                                                                                                                                                                                                                                                                                                                                       47 GluValValPheGlyLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal
                                                                                                                                                                                                                                                                                                                                                                      151 GGTCTCGCGTTAGGACTTTGTTTGTACTCCTGTGCGACGATAGGTACTTCTAATAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beet yellows virus Californian isolate, complete genome
AF056575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lirear
                                                    612
32
32
84
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses, ssRNA positive-strand viruses, no Closteroviridae, Closterovirus.
1 (bases 1 to 15468)
                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 (7), 5870-5876 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValSerAsnLeuArgGlnLeuGlyArg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAACTAGTTTGAAACAGCTGGGTCGT 594
                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  фç
                                                                                                                                                                      (1-612)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases : to 15468)
Dolja,V., Peremyslov,V. and
Direct Submission
                                                                                                                                                                      x BYU71295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF056575.1 GI:3283076
                                                    1.09e-22
296.00
54.50%
37.57%
29.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant closterovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beet yellows virus
Beet yellows virus
                                                                                                                                                                      US-09-613-486-15 (1-198)
                                                                                                     Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Virol.
98285746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF056575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9621048
                                                                                  Percent Similarity:
Best Local Similari
                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451
                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWCRDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
AF056575
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qC
                                                                                                                                                                                                    ò
                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                             55
                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                              55
                                                                                                                                                                                                                                                                                                                                                                                                      \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                          13731 AAACTACGGAGGATTTCGAAGGCTTTGAAAITGAAAITGAAAGGGGTTCCGGAAGATAAAACTC 13790
                                                                                                                                                                      13910
                                                                                                                                                                                                                                     13970
                                                                                                                                                                                                                                                                                                         14030
                                                                                                                                                                                                                                                                                                                                                                     14031 TACCGAGGAGACTGCCTCCGATTGCTAGAGCCAACCGTCACGGTCTACCTGCTGAAGAT 14090
                                                                                                                                                                                                                                                                                                                                                                                                                                       14091 CACTÁCTTAGCTGCTGATTTCATATCGACATCAACAGAACTTACTGACCTACAAGAAGGT 14150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14151 CGTCTGCTGTTGGCGCGCGAAAACGCCACTCACACAGAATTCTCG---TCTGAATCACCA 14207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="coat protein"
/protein id="AABi7001.1"
/brotein id="AABi7001.1"
/db xref="G1:16:1940"
/translation="MGSAEPISATFENVSJVDQTCLHGEDCDKLRRNFEECLKLKG
vPEDKLGALGLCLYSCATIGTSNKVSVQPPSTFIXASFGSGKELFTHGEIRSFLDS
QKLLEGKPNKLRCFCRTFQKDYISFAKEYRGRLPPIARANRHCLPAEDHYLAADFIST
STELTDLQQGRLLLARENATHTEFSSDSPVTSLKQLGRGLATGD"
                                                                                                   13791 GGTCTCGCGTTAGGACTTTGTTGTACTCCTGTGCGACGATAGGTACTTCTAATAAAGTT 13850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-CCT-1996
                                                                                                                                                                                                                                                                                                                                       145
                                                                                                                                                                                                                                                                        106 AsniyşieuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCys:leAla 125
                                                                                                                                                                                                                                                                                                                                                                                                        SerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2. (bases I to 612)
Creamer, R., He.X.H., Yang, C.H. and Grantham, G.
Direct Submission
Submitted (19-5EF-1996) Plant Pathology, University of California,
Riverside, CA 92521, USA
Location/Qualifiers
                                                                      99
                                                                                                                                   GlnArgAlaAspSerAspValllePheSerAsnSerPheGlyGlu---ArgAsnValVal 85
LeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIle 46
                                                                                                                                                                                                                         13971 AACAAATTGCGGTGTTTCTGCCGCACTTTCAGAAGGATTACATATCCTTCGCGAAGGAA
                                                                                                                                                                                                                                                                                                                                     TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlylleProAlaGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrPro
                                                                                                                                                                                                    ValThrGluGiyAspleuJysLysValLeuAspGlyCysAlaProLeuThrArgPheThr
                                                                    GluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Closteroviridae, Closterovirus.

1 (bases 1 to 6.2)

Creamer, R., He, X.H., Yang, C.H. and Grantham, G.

Characterization of the 3'-proximal encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BYU71295 612 bp RNA linear Beet yellows virus coat protein gene, partial cds. U71295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses, no DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Beet yellows virus"
/mol_type="genomic RNA"
/isolate="California BYV-CA"
/db_xref="taxon:12161"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 ValSerAsnLeuArgGinLeuGlyArg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l. .>612
/codcn_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yellows closterovirus
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U71295.1 GI:1619939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beet yellows virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beet yellows virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165
                                                                                                                                                                                                                                                                                                                                       126
                                                                                                                                                                                                                                                                                                                                                                                                         146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166
                                                                                                                                   67
                                                                    47
                                                                                                                                                                                                    86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BYU71295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEATURES
                                                                                                                                                                                                                                                                                                  00
                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
   ò
                                 00
                                                                  \delta
                                                                                                  QQ.
                                                                                                                                   ò
                                                                                                                                                                 DP
                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

270

83

210

99

46

90 26

390 145 450 165

oŧ

source

FEATURES

gene SCO

JOURNAL

```
protein_id="AAC25116.1"
db_xref="GI:3283078"
'translation="MDCVLRSYLLLAFGFWICLFLFCLVVFIWFVYKQILFRNTPPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSFTESCVNLSGYPCVXMVVEPSAAALSACSRIKGATSPVLVYDFGGGTFDVSVISAL
NNTFVVRASGGDMNLGGRDIDKAFVEHLYKKAQLPVNYKIDISFLKESLSKKVSFLNF
PVVSEQNVKVDVLVNVSELAEVAAPPVERTIKIVKEVYEKYRGSMRLEPSVKAKLLMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGDVALGNVGVSGSNTRTVPLTLEINVSSVGTITFSLVGPTGVKKLVSGNAAYDFSSY
QLGERVVADLHKHNSDKVKLIHALTYKPFQRKKLTEGDKALFLKRLSADYRREAGKFS
SYDDAVLNSSELLLGRVIPKILRGSRVEKLDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRESNGEVLSRKNFSDSTGESFVREFSLLLTFPKTYEVCKLCGVAMBQALSGMNRLSD
YNVSELNVVDVKTVGCKFNIQTVTEFVRKLNGNLAEPSLVBHCWSLSNSCGELINPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELIKVKVJSILITBON PELKLAQRWVGFHCYYGVFRTAQTRKVKRDAEYKLPPALGEFT
INMGSVEBEPPDLQKKMPSYGVRRRFCGSLGHERFSI FKRGYGRPPLTRLNVPYKYS
YLNVDYYRHVKRAGITGDELTILSN I FFDVAEMCCEREVALGARRAQRGEKPPGWKG
VKNEVSPHARSSI RYKRNRFELLINVIJMKDVGARRQGBLNPLHRRGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1,
/product="minor coat protein"
/protein_id="AAC25119.1"
/db_xref="GI:3283081"
/translation="MLAPEGRGDLIHFTEN"TRDAMETFFNSYDLAEYSEVNPNKLNRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETDELLGVIRERFKSELVITDEDFVKHLAFALIRAANITTSTKVNYVGAYEYTIGGKK
FLVKJAMVFPLIKECMKKFNKPNPVRTFCATFEDAYIVIARSLPKLFLNRTIGKRGIP
SGYEFLGADFLTATSVCLNDHEKAIVLQASRAAIDRAVSSSVDGKIVSLFDLGRLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MGSAEPISAIATFENVSLVDQTCLHGEDCDKLRRNFEECLKLKG
VPEDKLGLALGLCLYSCATIGTSNKVSVQPTSTFIKASFGSGKELFLTHGELRSFLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGSSYLPGLLSRLSSVPFVEECLVLPDARAAVAGGCALYSACLRNDSPXLLVDCAAHN
LSISSKYCESIVCVPAGTPIPFTGVRTVNMTGSNASAVYSAALFEGJFVKCRLNKRIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MTTRFSTPANYYWGELFRRFFGGREWKNLMSEAASVRRPVYDRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKRFVSLIFKGKDVVESTDEAVVSSSY.LDYLSHCLNLYETCN1.SSNSGKKALYDEFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVIVYLETSDLEYRSLSDNPLVAGVLYDMCFEYNTLKSTYLKNIESFDCFLSLYLFLL
SEIFSMNWEQPAPDVRLLFELDTTELLKIPTINTHDSTFLYKNKLRYLESYFEDDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEVAFGYDAEVLSNDPSVRGGFYRDLKRWIGCDEENYGDYLEKLKPHYKTELLKVAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MVVFGLDFGTTFSSVCAYVGEELYLFKQRDSAYIPTFVFLHSD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3KSTVRLDCYSGTVPQNATLPGLIATFVKALISTASEAFKCQCTGVICSVPANYNC
                                                                                                                                                                                                                                                                                                                                                                          note="ORF 1b; presumably expressed via a +1 ribosomal
                                                                                                                                                                   product="putative methyltransferase and RNA helicase"
note="ORF la"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="ORF 2; p6; small hydrophobic protein" codon start=1 product="6.4 kDa protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="homolog of HSP70 proteins; ORF 3"
                                                                                                                                                                                                                                                                                                                                      RNA polymerase"
                                                    function="replication enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13641. .14255
/note="22 kDa protein; ORF 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="major coat protein"
protein_id="AAC25120.1"
db_xref="G1:3283082"
                        function="autoproteclysis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12920. .13573
'note="24 kDa protein; ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product="64 kDa protein"
'protein_id="AAC25118.1"
'db_xref="G1:3283086"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
product="65-kDa_protein"
protein_id="AAC25117.1"
db_xref="G1:3283079"
                                                                                                                                                                                                                                                                                                                                      product = "RNA-dependent
                                                                                                                                                                                                               note="ORF ia"
oin(7983,8045. .9378)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11311. .12972
/function="unknown"
/note="ORF 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    445. .9609
function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9609. .11405
/function="unknown"
                                                                                                                                  gene="ORFla/b"
                                                                                                                                                                                                                                                                                             qene="CRF1a/b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                           rameshift"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARFNRSTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                        9445.
                                                                                                 mat_peptide
                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                SCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREDXTLKTELSGYDITYLDAKFVSRVFDYVGNCSVVNSKTFEWWGYTKSSKSRVV
ISGXVIRRDVHIDLKHSECFAAVMLAVGVRSRTTTETLAKNINYYTGDASCFETIRFL
ISGXVIRRDVHIDLKHSEFCKFAVMLAVGVRSRTTTETLAKNINYYTGDASCFETIRFL
ISGXVIRRDVHIDLKHSEFCKFAVMLAVGVRSRTTTFELDNSLQHLLEYSEVEVRSTRFL
EVOCREENRVLIFI TABAADRASIAGOLLSGALSSVPTOPRGGLRGGSRRGVSFLYNJ
VEEVGNLFFSVGDAVRFLVKVPKTFSDSPIFRVVRMFLDLABAASFFVSVVSLCAWLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAVSAFS SWVADRTVSES VKTFVNRTVKRFLNFMSAKTLTKKFFFFFLSASALAKTVY
KRACVILLEAM SKORLLPPSPSANTTEV
LLDLAKTKISTEN SKORLSPSSANTTEV
LLDLAKTKISTEN SKORLSPSSANTTEV
LPVFVRKCVALCVPGDMATYARFLEYGVDDLFFLGRSVNSIKNYGELGFTKVTLCG
LPVFVRKCVALCVPGDMATYARFLEYGVDDLFFLGRSVNSIKNYLCVVAAGLVOSIV
SKOKLSKORVAKRVLGFRFKIINFLAKTVYTPTSSTDLSEDSYFSODESKPG
LROGSSRFTLSKLLID FFNFKSSKLVJFRKAKVTFTSSTDLSPSFSODESKPG
RROGSSRFTLSKLLID FFNFKSSKLVJFNACFSARFIERNMKLYFFPLNSSEEBAR
RLIRCAGDFDYLSGSAFDEDEMLRQAFEQYYSSDDESVTYDGKFTVLKSVLNSSEEBAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFFFPEEPKKDKAKGASLPTKDEGFITFGTLRFPLSETPKEEPRLPKFREVEIPVVKK
HAVPAVVSKPVRTFRPVATTGAEYVNARTQCSRRPRNHPILKSASYTFGFKKMPLORF
MKEKKDYYVKRSKVVSSCSVTKSPLEALTSILKNLPRYSYNSERLKFYDHFIGDDFEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVHPLRGGKLSVLLILPKGEAYCVVTAATPQYHAALTIARGDRPRVGELLQYRPGEGL
CYAAIAALCCALQXRTPREEDFFVGWPYPTKPYBRYRDK
LPHCDVASAFSSPPYS.DRFTGGVEEBAPETTSSLKHKAIESVRSVSTHKDNLLARS
VEKOLIDFKDEIKSLSKEKRSVTVPFYMGEAVOSGLTRAYPQFNLSFTHSVYSDHPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGSRLLENETLASMAKSSFSDIGGCPLFHIKRGSTDYHVCRPTYDYKDAGRRYSRELQ
ARGLVENLSREQLVEAGARVSVCPHTLGNCNVKSDVLIMVQYYDASLNEIASAMYLKE
SKVAYLTMYTFGELLDEREAFAIDALGCDVVVDTRRDXVQYKFGSSCYCHKLSNIKNI
MLTPAFTFSGNLFSVEWYENRXGVNYYKITRSAYSPEIRGVKTLRYRRACTEVVQVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETFCNGPKFFVKVSNYFKALYSRLLRVLPWVDRNLSDSPGLKGGNEKALLAKFLKTCV
ITACECVSQICCLRLIRLCWGTPACGLVRLFYITYSGTRVLSRVVVAVAVCPLLVRNE
LDGLSDGLTNMGVSVPRRLFVALRRALSAYSNSALRRKIFEFIFGNIHHPFDVAVIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEVAPEPLSPEVDIDVDCDFGSDSESYSSDEVASIPRFGLHGGSRRSGNFLTGLVKVV
FKJACRIPRLJFRLENFVAYFVERRLASKRLKTFIGLARJFDNFSLTSVVYLLGEYDS
VLNAFIDVELVJJNSGSVNVLPLVSKVRGSLTKLAEVIVGSGFASFLGRXCCRVSDWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSSSNAGCNFMSPVRTKGKFVPPSSGGTASMYERLEALESDTREHVLSTCRVGSDEE
ERRENKELPERPOLEHTSBDVPTRSHSQPLSGGDESYSBDREHSRANLJ-FHVSKTVSE
RRGIEJTARRKKRTLGGOSEFLWAINTSNBQPRPIIVHSPEGRALTNSVREFYYLGEJ
ALFELSCKLREYYDQLKVANFNRQECLCDKDEDMFVLRAGQGTVSGRNSRLPLEAHFOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEFCFRSGGLVPYDGTSRVDTIFHTQTNFVSANALLSGYLSYRTFTFTNLSANVLLYE
APPGGGKTTTLIKVFCETFSKVNSLILTANKSSREEILAKVNRIVLDEGDTPLQTRDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEMGTQVFESGADNVVIRDSAPVNKSTDHEENLYSYESRNYNFTVCERFSGPOEFGOA
MAMVMLERSFDLEKVAKVRSDVIAITEKGVRTWMSKREPSQLRALSSDLQKPLNLEEE
ITTFKLMVKRDAKVKLDSSCLVKHPPAQNIMFHRKAVNAIFSPCFDEFKNRVITCTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NELDTAVLSDINRFVDDESRVYGEVSYRCPWDVCAWLSTFYPKTVATTNLVSAGGSSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKVNLVRTKFQEDDPFRSENHITVALSRHVESLTYSVLSSKRDDAIAÇAIVKAKQLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEDLLDVWWQGEYTSNATTLDQQLSFSVDNQRKSGASNTWIGNSIVTLGILSMFYYTN
RFKALFVSGDDSLIFSESPIRNSADAWCTELGFETKFLTPSVPYFCSKFFVMTGHOVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGDTYAALCAIHCIRSNFSSFKKLYPKVKGWVVHYGKLKFVLRKFANGFREKFDTAFS
EAYFLTYDET"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MAFLNVSAVPSCAFAPAFAPHAGASPIVPESFPCVPRYSDDISH
FRLTLS:.DFSVPRPLFLNARVHLRASTDNPLPSLPLGFHAETFVLELNGSSAPFSIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHIDFVVNRPFSVFPTEVLSVSSLRTPSRLFALLCDFFLYCSKPGPCVEIASFSTPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALGVTSKPNSRPITVKSASGEKYBAYEISRKDFERSRRÇQTPRVRSHKPRKINKAVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILTIDSYLMNNRGLTCKVLYLDECFWVHAGAAVACIEFTKCDSAILFGDSRQIHYIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVREI ESVDDVEYSSEFVYLTMLQSEKKDLLKSFGKRSRSSVEKPTVLTVHEAQGETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AYRVYPISFGGSTLDISVNPSISDRSKCKASSAPYEVINSFLESVVPGTTSVDFGDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIVFFTEMTNSTLASIAKEMLGSEHVYNVGEIDFSKFDKSQDAFIKSFERTLYSAFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVPDPYKLLVKLGASKDEVDDEFLFEVFTSFRDLTKDLVDERVIELLTHLVHSKYGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLVSNCVAQI PTHAEMESI RFPTKTLPAGRLLQFHKRKYTKRPETLI I HESGLALKTS
Submitted (31-MAR-1998) Botany and Plant Pathology, Oregon State University, 2082 Cordley Hall, Corvallis, OR 97331, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108. .1871
/gene="ORF1a/b"
/product="papain-like leader peptide"
                                                                                                                                                              'crganism="Beet yellows virus"
                                                                                                                                                                                                                                                                                                                                                                                               join(108. .7983,8345. .9381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="fusion_protein"
/protein_id="AAC25115.1"
/db_xref="GI:3283077"
                                                                                                                                                                                                   /mol_type="genomic RNA"
/isolate="Californian"
                                                                                                                                                                                                                                                                                 db_xref="taxon:12161"
                                                                                                                                                                                                                                                                                                                                                              'gene="ORFla/b"
                                                                                                                      .15468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
```

```
ETDELLGVIRERFKSELVITDEDFVKHLAFALIRAGNITTSTKVNYVGAYEYTIGGKK
FLVKDAWVFPLIKECMKKFNKPNPVRTFCATFEDAYIVIARSLPKLNLNRTIGKRGIP
SGYEFLGADFLTATSVCLNDHEKAIVLQASRAAIDRAVSSSVDGKIVSLFDLGRLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAA72955.1"
/db_xref="G1:323240"
/tanslation="MGSABITSAIATFENVSLADQTCLHGEDCDKLRKNFEECLKLKG
/translation="MGSABITSAIATFENVSLADQTCLHGEDCDKLRKNFEECLKLKG
VEFBUGLALGLCLYSCATIGTSNKVSVQPTSTFIKASFGGKELFLTHGELRSFLDS
QKLLEGKPNKLRCFGTFQKDYISPKEYRGRLPPIARANRHGLPAEDHYLAADFIST
STELTDLQQGRLLLARENATHTEFSSESPVTSLKQLGRGLATGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGROVVESTDEAVYSSYLDYLSHCIMLYETCMLSSNGGKKALYDEFLKYVIAYLETS
DLEYRSPSDNPLVAGVLYDMCFEYNTLKSTYLKNIESFDCFLSLYLPLLSEIFSMNWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPAPDVRLLFELDTABLLLKIPTINTLDSTFLYKNKLRYLESYFEDDSNELIKVKVDS
LLTRDNPELTALAQRAVGEHVYKOVFRAQRKKVKRABAKYLEPALGETINGSVEEF
EDELQKKKPSYSVRRFCGSLSHEAFSIFKREGVGEPPITRLAVPVKYSYLNVDYYRH
VKRAGLIQDELTILSNIEFDVAEMCCEREVALQARRAQRGEKPPQGWKGVKNEVSPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=ORF 2
/protein_id="AAA72954.1"
/db_xref="G1.23239"
/txanslation="MLAPEGRGDLIHFTENTRDAMETFFNSYDLAEYSBVNPNKLNRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="PDFVRKLNGNLAEPSLVEHCWSLSNSCGELINPKDTKRFVSLIF
                                                                                                                            C2-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerAsnLeuSerAsnLeuValIleThrAspAlaSerSerLeuAsnGlyValAspLysLys 26
                                                                                                                                             two CRFs.
                                                                                                                                                                                                                                                                                                                                                                                                           to genomic RNA
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                          VRL
                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                    stage;
                                                                                                             פוזיעערייט 2724 bp ss-RNA linear
Beet yellows virus coat protein gene, complete cds,
M59452
                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2724
71
31
85
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSSIRVKKSNESILNILWKDVGARRQGRLNPLHRKH"
                                                                                                                                                                                                                                                                                                                                                COat
                                                                                                                                                                                                                                                                                                                                                                                                       Original source text: Beet yellows virus cDNA Location/Qualifiers
                                                                                                                                                                                                                                                                    90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                     Brunstedt, J., Moseley, J. and Hull, R.
Nucleotide sequence of cDNA encoding the
yellows virus
                                                                                                                                                                                                                                                                Viruses, ssRNA positive-strand viruses,
Closteroviridae, Closterovirus.
1 (bases 1 to 2724)
                                            14234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAA72953.1"
/db_xref="G1:323238"
      ValSerAsnLeuArgGlnLeuGlyArg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Beet yellows
/mol_type="genomic RNA"
/isolate="Broom's barn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="coat protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-613-486-15 (1-198) x BYVVCPG (1-2724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:12161"
                           φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1956. .2570
/codon_start=1
/label=ORF 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/label=ORF_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /ccdon_start=1
/label=ORF 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.64e-21
293.00
53.97%
37.57%
29.57%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1885
                                                                                                                                                                                  M59452.1 GI:323237
                                                                                                                                                                                                                          Beet yellows virus
Beet yellows virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1287
                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1990)
                                                                                                                                                                                                          coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scores:
      186
                                            14208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Source
                                                                                                                                                                                                                                             CEGANISM
                                                                                                                          LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment
                                                                                                                                                                                                                                                                                                                                                                                    CCURNAL
                                                                                                                                                                                                     KEYWORDS
SOJRCE
                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                    RESULT 9
                                     Ω.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14031 TACCGAGGAAGACTGCCTCCGATTGCTAGAGCCAACCGTCACGGTCTACCTGCTGAAGAT 14093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13731 AAACTACGGAGGAATTTCGAAGAGTGTTTGAAATTGAAAGGGGGTTCCGGAAGATAAACTC 13790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4091 CACTACTTAGCTGCTGATTTCATATCGACATCAACAGAACTTACTGACCTACAACAAGGT 14150
                                                                                                                                                                                                                                                                                                                     /codon start=1
/product="21 kDa protein"
/product="21 kDa protein"
/product="21 kDa protein"
/db xref="GI:3283684"
/translation="MKFFFNDCETSRAISRSESLLRRVKELGTNSPQSEVSECINEFN
ELARENHLLVTVEHRERMEKHPKQSSELRTFSRLGEMLKEIRAFLKVRVVTPMHKETA
SSTLNARLESYCRITGLTREDALREKMRKVRSTVLFHHSELLKFEVTENXFSFTELLK
                                                                                                                                                                          /translation="MTSSVELAQTKPLFRVLLLKGFVPYIVAIFTEEESPEYELPLVY
LHDLELNVNKKGKIESSYIDFXSCMTELKPSSYSYTRYSSGKPSEDFSSSYSGKTFDS
KILNRKVTFTFESGIQLVFGMYGRDQRCVSSEYLWFENVFVGAHCGTLPYCLNCELDX
SGGELEILTFSKNEVFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145
XKLLEGKPNKLRCFCRTFQKDYISFAKEYRGRLPPIARANRHGLPAEDHYLAADFIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrPro 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 GlnArgAlaAspSerAspValllePheSerAsnSerPheGlyGlu---ArgAsnValVal 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 SerAsnLeuSerAsnLeuValIleThrAspAlaSerSerLeuAsnGiyValAspLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 LeuleuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGly1le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 ValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaProleuThrArgPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 AsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCysIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 GluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal
                       STELTDLQQGRLLLARENATHTEFSSESPVTSLKQLGRGLATGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15468
71
31
85
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                        14769. .15302 //function="replication enhancer" /note="ORF 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4426
                                                                                                     /codon_start=1
product="20 kDa protein"
protein_id="AAC25121.1"
/db_xref="GI:3283083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-613-486-15 (1-198) x AFC56575 (1-15468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                               function="unknown"
frote="ORF 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3696 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNESERVISSQIEGIAV"
3472 c 3696 a
                                            .4252. .14785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.93e-21
295.00
53.97%
37.57%
29.77%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNT
                                                                                                                                                                                                                                                                CDS
                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE CO
```

Score:

ò O,C 8 Ω̈́ ò Ω̈́ ò g ò g ò g ò 원 ç ΩD

CD.

ठे

CP

ò

D. 3 55 ò a ò a ò ρ ò

ò

```
GGSSYLPGILSRLSSVPFVEECLVLPDARAAVAGGCALYSACIRNDSPMILVDCAAHN
LSISSKYCESIVCVPAGSPIPFTGVRTVNMTGSNASAVYSAALFEGDFVKCRLNKRIF
SOPALGOVGSNTRTVPLTLEINVSSVGTITFSLVGPTGVKKLVGGNAAYDFSSY
OLGERVVADVHKHNSDKVKLIHALTYKPFQRKKLTDSDKALFLKRLSADYRREARFS
SYDAVLNSSELLLGRVIFKIIRGSRVEKLDV"
1937. .3598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon start=1
/potein.id="CAS1862.1"
/db_xref="G18.13695"
/db_xref="G18.13695"
/db_xref="SPTREMBL:Q65897"
/db_xref="SPTREMBL:Q65
                                                                                                                                         /db_xref="SPTREMBL:Q65893"
/translation="MDCVLRSYLLLAFGFLICLFLFCLVVFIWFVXKQILFRNNPPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEVAFGYDAEVLSNDSSVRGGFYRDLKRWIGCDEENVOOYLEKLKRHYKTELLKVAQS
SKSTVKLDOYSGTVPONATLPGLIATFVKALISTASERFKCCTGVICSVPANYNCLO
SKSTVKLDOYSGTVPONATLPGLIATFVKALISTASERFKCCTTGVICSVPANYNCLO
NNTFVVRASGGODWLGGRDIDENSFWHLYKKAQLFVYFYBGGGSTFDVSVISAL
NNTFVVRASGGDWMLGGRDIDENSFWHLYKKAQLFVYKKIDISFLKSGLSKKVSFLNF
PVVSEQNVKVDVLVNVSELAEVAAPFVENTIKIVNBVYEKYRGSMRLEPSVKAKLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="coat protein homolog"
/protein id="CAA51860.1"
/db_xref="101:31393"
/db_xref="101:31393"
/db_xref="SPTERMBL:065896"
/translation="WLASEGRGDLIHFTENTRDAMETFNSYDLAEYSEVNPWKLNRX
FIDELLGVIRERFKSELVIDDEPVWHAFALIHAANITTSTKWNYVGAYSYTIGGKK
FLYKDAWYFPIKENGKKKRNRNPWTFCAFFEDAYIVIAA5LENKTIGGKK
FLYKDAWYFPIKENGKKKRNRNPWTFCAFFEDAYIVIAA5LENKTIGGKG
FLYKDAWYFPIKENGKRKKRNRNPWTFCAFFEDAYIVIAA5LENKTIGKK
FLYKDAMPTATSVCLNDHEKAIVLOASRAAIDRAVSSSVDGKIVSLFDLGRLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xxef="SPTREMEL:003724"
/translation="WGSAED:SAIATFENVS.ADQTC.HGECCDKLRKYFEBCLKLKG
VFEDKLGLALGLCLYSCATIGTSNKVSVQPTSTFIKASFGGGKELF1THGELRSFLDS
QKLLEGKPNKLRCFGTTFQKEYISPKEYRGRLFPTARANRHGLPAEDHYLAADFIST
STELTDLQQGRLLLARENATHTEFSSESPVTSLKQLGRGLATGR"
                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref。"SPTREMBL:Q65894"
/translation="MVVFGLDFGTTFSSVCAYVGEELYLFKQRDSAYIPTFVFLHSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLNVDYYRHVKRAGLTQDELTILSNI EFDVAEMCCERBVALQARRAQRREKPFQGWKG
VRNEVSPFARSSIRVKKSNESLLNI LWKDVGVRRQGRLNPLARKH"
   'note="putative membrane-binding protein"
                                                                                                                                                                                                                                                                                                                /product="heat shock 7C-related protein"
/protein_id="CAA51858.1"
/db_xreff="GI:313691"
                                                                        /protein_id="CAA51857.1"
/db_xref="GI:313690"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="coat protein"
/protein_id="CAA51861.1"
/db_xref="GI:313694"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5395. .5928
/note="orf8"
/codon_start=1
                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="orf4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4878. .5411
/note="orf7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3546. .4196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4881
                                                                                                                                                                                                           EARFNRSTVV
                                                                                                                                                                                                                                               SCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BYVMBPA 10-00T-1993 Beet yellows virus (isolate German BYV-G) genes for putative membrane-binding protein, heat shock 70-related protein, coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agranovsky, A.A., Koomin, E.Y., Boyko, V.P., Maiss, E., Lunina, N.A. and Atabekov, J.G.
2106 GGTCTCGCGTTAGGACTTTGTTTGTATTCCTGTGCGACGATAGGTACTTCTAATAAGTT 2165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2466 CGTCTGCTGTTGGCGCGCGAAAACGCCACTCACACAGAGTTCTCG---TCTGAATCACCA 2522
                                                                                                                                                                                                                                                                                                                                                                                                                                           2286 AACAAGTIGGGITGTIICIGGGGACTITICAGAAGGACTACATATCCTTGGGGAAGGAA 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgiysMetPheAlaSerMetTyrAlaLeuiysThrGluGlyGlyValValAsnThrPro 185
                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                 85
                                                                                                 LeuLeuSerAlaGluValGluLysMetLeuValGlnJysGlyAlaProAsnGluGlylle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2406 CACTACTTAGCTGCTGATTTCATATCGACATCAACAGAACTTACTGACCTACAACAACAAGA
                                                                                                                                                               2046 AAACTACGGAAGAATTTCGAAGAGTGTTTGAAATTGAAAGGGGTTCCGGAAGACAACTC
                                                                                                                                                                                                                                                                                                                                                                          67 GinArgAlaAspSerAspValllePheSerAsnSerPhe---GlyGluArgAsnValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaProLeuThrArgPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCyslleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 SerTyrbeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer
                                                                                                                                                                                                                                        47 GluValValPheGlyLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fuer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      und
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-JUN-1993) E. Maiss, Inst. f. Biochemie und
Pflanzenvirologie, Biologische Bundesanstaldt, Institut
Biochemie, Messeweg 11/12 D-3300 Braunschweig, FRG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beet yellows closterovirus: complete genome structure identification of a leader papain-like thiol protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beet yellows virus
Beet yellows virus
Viruses, seRNA positive-strand viruses, no DNA stage;
Closteroviridae; Closterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Bee: yellows virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /moi_type="genomic_RNA"
/isolate="German (BYV0G)"
/db_xref="taxon:12161"
/clone="pBYV-D22, pBYV-D31"
71. .235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 5980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (18-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maiss, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166
                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BYVWBPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
```

RESULT

g

ò

SOURCE

```
/codon_start=3
/product="RNA_polymerase"
/protein_id="CAA37549.1"
/db_xref="GI:80847"
/db_xref="SPTREMBL:Q66109"
/translation="DNQRKGGASN"WIGNSIETLGILSMFYYTNRFKALFVGGDDSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSESPIRNSADAMCTELGFETKFLTPSVPYFCSKFFVMTGHDVFFVPDPYKLLVKLGA
SKDEVDDEFLFEVFTSFRDLTKDLVDERVIELLTHLVHSKYGYESGDTYAALCAIHCI
RSNFSSFKKLYPKVKGWVVHYGKLKFVLRKFANCFREKFDTAFGERTFLLTTKLETVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSFTESCVNLSGYPCVYMVNEPSAAALSACSRIKGATSPVLVYDFGGGTFDVSVISAL
NTTFVRASGODMULGGRDIDGAFVEHLYNKAQLPHYNKTDISFEXKESLSKKVSELNF
NTTFVRASGOGRAUDVLNYVSELARVAAEFVERTIKIVKEVYEKYCSSMELEPUVKAKLLMV
GGSSYLPGLLSRLSRIPFVDECLVLPDARAAVAGGCALYSACLIRNESPMLLVDCAAMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="myvfcudegytessycayvgeelylekordsayiptyvelhsdd
Qevargydaevlsndlsvrggfyrdlkrwigcdeenyrdyleklkphyktellkvaqs
Skstvkldcysgtvpqnatlpgliatfvkalistaseafkcqctgvicsvpanynclq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSISSKYCESIVCVPAGSPIPFTGVRTVNMTGSNASAVYSAALFEGDFVKCRLNKRIF
FGDVVLGNVGVTGSATRTVPLTLEINVSSVGTISFSLVGPTGVKKLIGGNAAYDFSSY
QLGERVVADLHKHNSDKVKLIHALTYQPFQRKKLTDGDKALFLKRL,ADYRREARKFS
                        Agranovsky, A.A., Boyko, V.P., Karasev, A.V., Lunina, N.A., Kocnin, E.V. and Dolja, V.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MDCVLRSYLLLAFGFLICLFLFCLVVFIWFVYKQILFRTTAQSN
                                                                                                     closterovirus RNA genome: unique arrangement of eight virus genes
7. Gen. Virol. 72 (Pt 1), 15-23 (1991)
911.6305
                                                                                 beet yellows
                                                                                                                                                                                                                                                             Putative 65 kDa protein of beet yellows closterovirus is
homologue of HSP70 heat shock proteins
J. Mol. Biol. 217 (4), 603-610 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-MAY-1990) Agranovsky A.A., A.N. Belozersky Laboratory, Moskow State University, Moskow 119899, USSR 5 (bases 2678 to 6746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-JUL-1990) Agranovsky A.A., A.N. Belozersky
Laboratory, Moskow State University, Moskow 119899, USSR
                                                                                                                                                                                           2 (bases 1 to 6746)
Agranovsky, A.A., Boyko, V.P., Karasev, A.V., Koonin, E.V.
                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 6746)
Rensing, S.A. and Maler, U.G.
Phylogenetic analysis of the stress-70 protein family 94343547
                                                                               Nucleotide sequence of the 3'-terminal half of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYDDAVLNSSELLLGRIIPKILRGSRVEKLDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Beet yellows virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="HSP70 homologue"
/protein_id="CAA37551.1"
/db_xref="G1:58880"
/db_xref="SWISS-PROT:P37092"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /proteIn_id="CAA37550.1"
/db_xref="G1:58879"
/db_xref="SPTREMBL:Q08542"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic RNA"
/db_xref="taxon:12161"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="ORF2"
              (bases 1 to 6746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 2677)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARHINHSTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .6746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lirect Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agranovsky, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agranovsky, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            710.
                                                                                                                                                                                                                                            Dolja, V. V
                                                                                                                                                                                                                                                                                                                                91171285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7545947
                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                MEDLINE
PUBMED
                                 AUTHORS
                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                   PUBMED
                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JCURNAL
                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                          TITLE
                                                                                                                                                                                                                                                               TITLE
                                                                     /translation="MKPFFNDGETSRAISRSBSLLRRVKELGTNSPQSEVSECINEFN
THARTHLUTVTVEHREWMEKHPKQSSBLRAPSRLGBMLKEIRAFLKVRVVTPYHKETA
SETLNAFLLDTYCRIAGLTREDALREKWRKVRSTVLFHKSELLKFEVTENMFSFTELLK
LNLSLRVISSQ1.GAIAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4357 AAACTACGGAAGAATTTCGAAGAGTGTTTAAAATTGAAAGGGGTTCCGGAAGACAACTC 4416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLBYV3PH
Beet yellows virus genome 3'-proximal half, for capsid protein
HSP70 related protein, RNA-dependent RNA polymerase and ORFs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAsp 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 ValThrGluG, yAspLeuLysLysValLeuAspGlyCysAlaProLeuThrArgPheThr 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 SerTyrieuAlaAspPheLeuGlyThrCysProlysLeuSerGluLeuGlnGlnSer 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 SerAsnLeuSerAsnLeuVallleThrAspAlaSerSerLeuAsnGlyValAspLysLys 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 GlnArgAlaAspSerAspValllePheSerAsnSerPhe---GlyGluArgAsnValVal 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X53462.. GI:58878
capsid protein; heat shock protein 70 homologue; RNA polymerase;
RNA-dependent RNA polymerase; unidentified reading frame.
Bet yellows virus
Beet yellows virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 LeuleuSerAlaGluValGlulysMetLeuValGluLysGlyAlaProAsnGluGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 GluvalvalPheGiyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4417 GSTCTCGCGTTAGGACTTTGTTTGTATTCCTGTGCGACGATAGGTACTTCTAATAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 AsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCyslleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4597 AACAAGTIGCGIIGTIICTGCCGCACTTITCAGAAGACTACATATCCTICGCGAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4657 TACCGAGGAAGACTGCCTCCGATTGCTAGAGCCAACCGTCACGGTCTACCTGCTGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 ArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4777 cercrecrerredecececeaaaceceacreacheagricres---regaarcach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5980
71
31
85
2
                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
/protein_id="CAA51863.1"
/db_xref="G1:313696"
/db_xref="SPTREMBL:Q65898"
                                                                                                                                         :LGIAV"
1431 g 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4834 GTAACTAGTTTGAAACAGCTGGGTCGT 4860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 ValSerAsnLeuArgGlnLeuGlyArg 194
                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-613-486-15 (1-198) x BYVMBPA (1-5980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Closteroviridae; Closterovirus.
                                                                                                                                                                                                                                                          4.64e-21
                                                                                                                                                                                                                                                                                293.00
53.97%
37.57%
29.57%
                                                                                                                                                            1267 C
                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                   α
                                                                                                                                                               1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X53462
                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Locus
DEFINITION
                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                            BASE CCUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLBYV3 PH
                                                                                                                                                                                       CRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
```

qq

8

g े a

ò

ò

ਨ ch Ch à g ò g ò G $\ddot{\varsigma}$ O,

8

99

46

5235

5355

165

145

```
/mol type="genomic RNA"
/isolate="Ukrainian (BRV-U)"
/db xref="taxon:12161"
/clone="pBYV p36, x19, R3, 36A, R2, 36, p43, 111-7, 112, 115, 1213, 1210, 124, 1313, 1311, 142, 143, 1311, 1311, 142, 143, 156, 1510, 154, 1518,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coat protein; heat shock 70-related protein; heat shock 90-related protein; methyltransferase; papain-like protease; RNA dependent RNA polymerase; RNA helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRL 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Belozersky Institute
                                                                                                                                                                                                                                                                                                                                                                           106 AsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCysIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 LeuLeuSerAlaGluValGluLysMetLeuValGlnLysSlyAlaProAsnGluGly1le
                                         1996 AAACTTAGGAAGAACTTCGAAGAGTGTTTGAAATTAAAAGGGGTTCCGGAAGATAAACCTC
                                                                                                                                                                                                                               86 ValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaProLeuThrArgPheThr
                                                                                                                                                                                                                                                                                                                                                                                                               5236 AACAAATTGCGGTGTTTCTGCCGTACTTTCAGAAGGACTACATATCCTTGCGCAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 SerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 ArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5416 CGTCTGCTGTTAGCGCGCGAAAACGCCACTCACACGGAATTCTCG---TCTGAATCACCG
                                                                                          47 GluValValPheGlyLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal
                                                                                                                                      5056 GGAATCGCGTTAGGACTTTGTTTTGTATTCCTGTGCTACGATAGGCACTTCCAACAAGTT
                                                                                                                                                                                   67 GlnArgAlaAspSerAspVaillePheSerAsnSerPhe---GlyGluArgAsnValVal
                                                                                                                                                                                                                                                                                                                            5176 CTCACTCACGGTGAATTGAATTCCTTTCTGGGGTCTCCAAAACCTTTTGGAGGGAAAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15480 bp RNA linear VRJ 19-MA
Beet yellows virus (isolate Ukrainian BYV-U) complete genome.
X73476
X73476.1 GZ:405624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agranovsky, A.A., Koonin, E.V., Boyko, V.P., Maiss, E., Frotschi, Lunina, N.A. and Atabekov, J.G. Beet yellows closterovirus: complete genome structure and identification of a leader papain-like thiol protease Virology 198 (1), 311-324 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (18-JUN-1993) A.A. Arganovsky, A.N. E
Moscow State University, 119899 Moscow, Russia
Related sequence: X53462.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .15480
/organism="Beet yellows virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5473 GTAACCAGTTTGAAACAACTAGGTCGT 5499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 ValSerAsnLeuArgGinLeuGlyArg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beet yellows virus
Beet yellows virus
Viruses; SRNA positive-strand
Closteroviridae; Closterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 15480)
Agranovsky, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94382464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8259666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCILINIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BYVUAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCURCE
                                                                                                                                                                                                                     C).
                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                े
                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="MGSABPISAIATFENVSLADQTCLHGEDCJXLRXNFEECJXLXG
VPEDNJGIALGLCLYSGATIGTSNKYNVQPTGTFIKASFGGGKELYLTHGELNSFLGS
CKLLEGKPNKLRCFCRTFQKDYISLRKEYRGKLPPTARANHGLPABJHYLAADFIST
STITTULQGKLLLARENATHTEFSSESPVTSLKQLGRGLGTGR"
/note="ORF?"
                                                                                                                                                                                                                          HVIDYLENSDLEYRSPSDNPLVAGILYDMCFEYNTLKSTYLGNISEROCFLSTLLEL
SEVFSMYWERPAPDVRLLFELDAAELLLKVPTINMHDSTFLYKNKLRYLSYFEDDSN
ELIKYKVDELTRDNPELKLAQRWVGHCYYQYRFRAQTRKVRRDAEYKLPPALGEFY
INNSGVEEFFEELGKMPPSISYRRRPGGSLSHEAFSVFKRFGOFPTTRLNVPVKYS
YLNVDYYRHYKRVGTTODELTILLSNIEFDVAENCCEREVALGARRAGRREKFFGSKKG
TKNEISPHARSIRVKKNDBLLNILMKDVGARSQRRLNPLHRKH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="XKFFLKDGETSRALSRSESLLRRVKELGTNSQQSEISECVDEFN
TALASRWLLTVTVEHREWMEQHFNQSSKLRVFCRTGEMLKEIRAFLKVRVVTPVHKETA
SDTLNAFLEFYCRITGLAREDALREKWRKVKSVVLFHHSELLKFEVTENMFSYTELLK
INLSLRVISSQ1LGMAT"
                                                                                                                                                        FRESDGVILSRKTFGESTGESFVREFSLLLTFPKTYEVCKLCGVAMELALNGKNRLSD
YNVSEFNIVDVKTVGCKFNIQSVTEFVKKINGNVAEPSLVEHCMSLSNSGGELINPKD
TKRFVSLIFKGKDLAESTDEAIVSSSYLDYLSHCLNLYFTCNLSSNSGKKSLYDFTLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MLAPEARGDLIFFTENTRDAMETFFNSYDLAEYSEVNFNKLNRK
EDELGGVIERERKSELVITDEDFVRHALAFALIFAANTTYTSVKNYVYORYSPYTJGKK
FLVKDAWVFPLIKECKKKKNKNPNPVRFCAFFEDATVITARSLFMEINRTIGSKR
FLVKDAWVFPLIKECKKKFNKNPNPRFCAFFEDATVITARSLFMEINRTIGSKRGIP
SGYEFLGADFLIATSVCLNDHEKAIVLQASRAAIDRAVSSSVDGKIVSLFDLGRLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LITERISIA ION = MYDSYBEAQTKPLFRVLLLKGFYFYVARFETEESSSABLPLVV
LITERININKGKIBASYDFMSCATTKPSSNSYTRVSEKSBDFSLPGSGKTTGS
KVARRVTFFERNOVLVFGMYGLEGRCVSSPYJMFBRVFVGAHGGTLTYCLKTSELB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4936 GCGACTTTTGAAAACGTAAGTCTCGCAGACCAAACCTGTTTGCACGAGAAAGACTGCGAT 4995
                                                                                                                                      translation="MTTRFSTPANYYWGELFRRFFGGQEWKNLMSEAASVSRFRYSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 SerAsnieuSerAsnieuVallieThrAspAlaSerSerLeuAsnGlyValAspLysLys 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6746
71
29
87
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1975 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/protein_id="CAA37556.1"
/db_xref="G1:58885"
/db_xref="SPTREMBL:Q08545"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=:
/protein_id="CAA37555.1"
/db_xref="GI:58884"
/db_xref="SPTREMBL:Q08544"
                                       /coden_start=1
/protein_id="CAA37552.1"
/db_xref="GI:58881"
/db_xref="SPTREWBL:Q66110"
                                                                                                                                                                                                                                                                                                                                                                                                                                          proteīn_id="CAA37553.1"
|db_xref="GI:58882"
|db_xref="SPTREMBL:008538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="capsid protein"
protein id="CAA37554.1"
/db_xref="GI:58883"
/db_xref="SPTREMBL:Q08531"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-613-486-15 (1-198) x CLBYV3PH (1-6746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGGELEILTFSKNEVLLKRW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1581 9
                                                                                                                                                                                                                                                                                                                                                                                                                       codor_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon start=1
                                                                                                                                                                                                                                                                                                                                                                           1185. .4835
/ncte="ORF5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5034. .6567
/rote="ORF8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C8e-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286.00
52.91%
37.57%
28.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1415 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

CDS

```
9608. .11404
/codon_start=1
/codon_start=1
/producf="heck 70-related protein"
/protein_id="cAA51865.1"
/db_xref="G1:405628"
/db_xref="SI:5S-ROT; P37092"
/translation="WVPFGLDFGTFSSVCAYVGEEJYEPCRDSAYz PTYVFLHSDTORPRGYDAEVLSNDLSVRGGFYRDLKRWIGCDEENYRDYLEKLKPHYKTELLKVAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNTFVVRASGSDANIGGRDIDKAFVEHLYNKAQLPVNYKIDISFLKESLSKKYSFLNF
PVVSEQGVRVDVLVNVSELAEVAAPFVERTIKIVKEVYEKYGSSARLEPNVKAKLLMV
GGSSYLPGLLSRLSSIPFVDECLVLPDARAAVAGGCALYSACLRNDSPMLLVDCAAHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSISSKYCESIVCVPAGSPIPFTGVRTVNMTGSNASÄVYSÄALFEGDFVKCRLNKRIF
EGDVLGAVGVTGSARTVBFLTLEINVSVGTISFSLVGFTGVKKLJGGNAAVDFSSY
QLGBRVVADLHKHNSDKVKLIHALTYQPFQRKKITDGDKALFLKRLTADYRREBARKFS
SYDDAVLNSSELLLGRIIPKILRGSRVEKLDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MTTRFSTPANYYWGELFRRFFGGGEWKNLMSEAASVSRPRYSSD
PRFCDGVILSRKTFGESTGESFVREFSLLLTPPKTYEVCKLGGVAMELALNGYMRLSD
YNVSERNIVOVKTVGCKFNIGSVTEFVKKINGNVAEPSLVEHCWSLSSNSCGELINPKD
YRRFVSLIFKGKDLABEAIVSSSYLDYLSHCKLNYFTCNLSSNSGKKSLYDEFLK
HVIDYLENSDLEYRSPSDNPLYAGILYDMCFFYNTLKSTYLKNIESFOCFLSIYLYLDLI
SEVFSMNWERPAPDVFLLFELDAAELLLKVPTINMHDSTFLYKNIESFCFLSIYLPLLI
SEVFSMNWERPAPDVFLLFELDAAELLLKVPTINMHDSTFLYKNIESYFEDDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="coat protein"
/product="coat protein"
/protein_id="CAA51868.1"
/db_xref="ed1:405631"
/db_xref="SPTREMBL.08531"
/db_xref="SPTREMBL.098531"
/translation="waSAEPISATATFENVSLADQTCLHGEDCDXLRKWFESCLKLKG
VPEDNLGIALGLCLYSCATIGTSNKVNVQPTSTFIKASFGGGKELYZTHGELNSFLGS
OKLLEGKRNKLRCFCRTFQQDYISLRKEYRGKLPPIARANNHGLPAEDHYLAADFIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/protein_id="CAA51869.1"
/db_xref="G1:405532"
/db_xref="SPTREMBL:008544"
/db_xref="SPTREMBL:008544"
/db_xrefin="MYSSVERAQTREFRVLLLKGFVFYVVAPETEEESSEAELPLVY
LHOPELN:NKRGKTEASYVDFMSGVTRLKPSSVSYTRVSSEKSEDFSLPGSGKTFGS
KVLNRKVTFTFENGVQLVFGMYGLEGARCVSSDYLWFENVFVGAHGGTLTYCLNCELDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELIKUKVDSLLTRDNPELKLAQRWVGFHCYYGVFRTAQTRKVKRDASYKLPPALGEFV
INNSGVEEFFEELQKKMPSISVRRFCGSLSHEAFSVFKRFGVGFPPITRLNVPVKYS
YLNVDYYRHVKRVGLTQDELTILSNIEFDVAEMCCEREVALQARRAQRGEKPFQGWKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="MLAPEARGDLIHFTENTRDAMETFPNSYDLAEYSEVNPNKLNRR
EDEBLIGV: RREFKSELVIDDEPVARILAFALIRAANITTSVKNYYVADAYEYTIOGKK
FLYKDAWVPPLIKEOWKKRPRENPRTFCATFEDA! VIARSLPKLELNRTIGKRGIP
SGYEPLGADFLIATSVCLNDHEKAIVLOASRAAIDRAVSSSVDGKIVSLFDLGELS
                                                                                                                                                                                                                                                                                                                           /db_xref="SPTREMBL:Q08542"
/translation="MDCVLRSYLLLAFGFLICLFLFCLVVFIWFVYKQILFRTTAQSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKSTVKLDCYSGTVPQNATLPGLIATFVKALISTASEAFKCQCTGVICSVPANYNCĽQ
RSFTESCVNLSGYPCVYMVNEPSAAALSACSRIKGATSPVLVYDFGGGTFDVSVISAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="putative heat shock 90-related protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKNBISPHARSSIRVKKNNDSLLNILWKDVGARSQRRLNPLHRKH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STELTDLQQSRLLLARENATHTEFSSESPVTSLKQLGRGLGTGR"
                                                                                                                                                                    'note="putative membrane-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12919. .13569

/codon_start=1

/product="coat protein homolog"

/protein_id="CAA51867.1"

/db_xref="G1:405630"

/db_xref="SPTREMBL:Q08538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA51866.1"
|db_xref="GI:405629"
|db_xref="SPTREMBL:QC8541"
                                                                                                                                                                                                                                   /protein_id="CAA51864.1"
/db_xref="GI:405627"
    045. .9393
gene="CRF1a/b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11310. .1297
                                                                                                                                                                                                                                                                                                                                                                                                               EARHNHSTVV"
                                                                                        number=
            coxe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RKAKVI LEAVREWREETLSBOGGEYSAVEFCSSVVITJITNSCRLLEPGFSPSAITTEV
LLDLATKI SIEVLLKQI SPADSTASSALYRRVLSEILSNFRTMGEHG; FTKVFLLCGF
LPPYRKCALCVPGEMATYARFLEYGVDDJSEILGSKYSIRYLCVAAG; VDSIVS
SVVLKLSGVAKERVLGFKATI KNFLNVFRKAKVVTRTSSSTDLSEDEYFSCDESKPG
LRGGSSFTLSRLLDFFFLKSSKLVI ENAGFSAVER; ERNMKLYFFPLNSSEERA
RLIRCAGDFDYLSDSAFDEDEMLRQAFEQYYSSDDESVTYJGKPTVLSSYLNVSREFA
ETFCNGPKFFVKVSNYFKALYSRLLRVLPWVDRYLSDSPGLKGGNEKALLAKFFKTÇV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPGGGCTTTLIKUSCETPSKVNSLILTANKSSREBILAKVNR VLDEGDT-LQTRDR
LLTIDSYLMNNRGLTCKVLYLDECFWYHAGAAVACIEFTKCDSALLFGDSRQIRYGRC
SPLDTRVLSDINRFVDDESRYYGBVSYRCPWDVCAMLSTFYRTVATTNLVSAGQSSM
CHUSTSKODVEYSSEFVYLTMLQSEKRDLKSFGKRSRSVEKPTVLTVHEAGGSTYRKVNLYTKTKPQEDPFRSENHITVALGSRAVESLTYSVLSSKEDDALAQAIVKKQLVD
AYRVYPTSFGGSTLDVSVNFSTSDRSKCKASSAPYEVINSFLESVVFGTTSVDFGDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYLAHAALCCALQKRTFREEDFFVGMYPTKFVFAKRLTEKLGFSALKHPVRGRQVSRS
LFHCDVASAFSSPFYSLPRFIGGVEEEAPEITSSLKHKAIESVYERVSIHKDNLLARS
VEKDLIDFKDEIKSLSKEKRSVTV?FYMGEAVQSGLTRAYPQFNLSFTHSVYSDHPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGSRLLENETLASMAKSSFSDIGGCPLFHIKRGSTDYHVCRPIYDXKJAQRRVSRELQ
ARGLYENLSREQLVEAQARVSPYTLAGNCNYSDDIJMYQYYDASLINEJASAMYLKE
SKVAYLTHYYTPGELJEBREAR JDAJGCDVYVJTRADNOVQYKFGSSCYCHKISKIKSI
MLTPAFTFSGNLFSVEMYENRXGVNYYKITRSAYSPEIRGVKTLEYRRACTEVVQYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVDCNEENRVLTEIIAEAADRKSIAQGLSGALSSVPTQPRGGLRGSSRRSGVSFLYNL
VEEVGNLFFSVGDAVRFLVKVFKTFSDSPIFRVVRMFLDLAEAASPFVSVVSLCAWLR
EAVSAFSSWVADRTVSESVKTFVNRTVKRFLNFMSAKTLTKKFFRFFLSASALAKTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITACECVSQICCLRLIRLCWGTPACGLVRLFYITYSSTRVLSRVVVAVAVCPLLVRNE
LOGGSDGLTHWGVSVFRLFYALRRALSASASNSABRRRKIEFET STENLHFPFDVANIET
NEVAPEPLSPEVDIVDDFGSDSSSVSDFVASNPRGLHGGSRRSSNFITSLVKVV
FKLARRIPRLLFRRNFVAXFVERRLASKRLKTFIGLARLFDNFSLTSVVYLLGSTDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLNAFIDVELILLNSGSVNVLPLVSWVRGSLTKLAEAIVGSGFASFLGRMCCRVSDMC
SSSSNAGCNFMSPVRTKGKFVPPSSSGSTASMYERLEALESDIREHVLSTCRVGSDEE
EERPKEVTEPGIEHTSEDVVPIRSHSQPLSGGECSYSEDREENBLALLPHVSKIVSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRGLETARRNKRTLHGVSEFLNAINTSNBQPRPIIVDHSPESRALTNSVREFYYJQEL
ALFELSCKLREYYDQLKVANFNRQECLCDKDEDMFVLRAGQGTVVSGRNSRLPLKHFKG
HEFCFRSGGLVPYDGTSRVDTIFHTQTNFVSANALLSGYLSYRTFTFTNLSANVJLYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFKALFVSGDDSLIFSESPIRNSADAMCTELGFETKFJJPSVPYFCSKFFVYJGHDVF
FVPDPYKLJVKLGASKDBVDDEFLFEVFTSFRDLTKDJVDERVIELJTHLVHSKYGYE
SGDTYAALCAIHCIRSNFSSFKKLYPKVKGWVVHYGKLKFVLRKFANCFREKFDTAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLVSNCVAQI PTHAEMESIR PPTKTIPAGRFI QPHKRKYTKRPETLI IHESGLALKTS
ALGVTSKPNSRPI TVKSASGEKYEAYE ISRKOPERSRRRQQT PRVRSHXPRKINKAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAVPAVVSKPVRTFRPVATTGAEYVNARNQCSRRPRNHPILRSASYTFGFKKMPLGRF
YKEKKEYYVKRSKVVSSCSVTKSPLEALASILKNLPQYSYNSBRLKFYDHFIGDDFBI
EVHPLRGGKLSVLLILPKGEAYCVVTAATPQYHAALTIARGDRPRVGELLQYRPGEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISGKVIHRDVHIJLKHSECFAAVMLAVGVRSRTTTEFLAKNLNYYTGDASCFETIRFL
FREWSRRAYAEINRSFRKLMKSILSAGLDYEFLJLDNSLQHLLEYSEVEVRVSIAÇNG
                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MAFLNVSAVPSCAFAPAFAPHAGASPIVPDSFPCVPRYSDDISH
FRLTLSLDFSVPRFLSLNARVHLSASTDNPLPSLPLGFHAETFVLELNGSSAPFSIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHIDFVVNRPFSVFPTEVLSVSSLRTPSRLFALLCDFFLYCSKPGPCVEIASFSTPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAMVMLERSFDLEKVAKVRSDVIAITEKGVRTWMSKREPSQLRALSSDLQKPLNLEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :TTFKLMVKRDAKVKLDSSCLVKHPPAONIMFHRKAVNAIPSPCFDEFKNRVITCTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEDLLDVWMQGEYTSNATTJDGQLSFSVDNQRKSGASNTWIGNSIETLGILSMFYYTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFFPEEPKKDKRKRASLPTEDEGFITFGTLRFPLSETPKEEPRLPKFREVEI PVVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRFDKTLKTFLSGYDYIYLDAKFVSRVFDYVVSNCSVVNSKTFEWVWSYIKSSKSRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EE%GTQVFESGADNVVIRDSAPVNKSTDHEENLYSYESRNYNFTVCERFSGPQEFGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIVEFTEMTNSTLASIAKEMLGSEHVYNVGEIDFSKFDKSQDAFIKSFERTLYSAFGF
                                                                                                                                                                                                 papin-like protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="+1 ribosomal frameshift signal"
                                                                                                                                                           /codon_start=1
/product="fusion_protein_of_papir
methyltransferase, RNA_helicase"
/protein_id="CAA51871.1"
/db_xref="GI.809539"
/db_xref="SPTREMBL:Q08534"
                                                               oin(108. .7983,8045. .9393)
gene="ORF1a/b"
.7983,8645. .9393)
                                     /gene="ORFla/b"
cin(108. .7983,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7983. .8045
/gene="ORFia/b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERTFLLTTKLETVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108. .7983
/gene="ORF1a/b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7984. .8044
/gene="CRFla/b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /nrmper=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
    gene
```

```
2.3e-21
285.00
53.44%
37.04%
Beet yellows virus
                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                           æ
                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166
                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
BYU51931
LOCUS
DEFINITION
                                                                                                                            source
                                                                                                                                                                       BASE COUNT
ORIGIN
ORGANISM
                                                                                                                                                                                                                           Pred. No.:
                                               AUTHORS
TITLE
JOURNAL
                                    REFERENCE
                                                                                                 CCMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            먑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                     ે
                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dC.
                                                                                                                                                                                                                                                                                                                            14150 CSTCTGCTGTTAGCGCGGAAAACGCCACTCACGGGAATTCTCG---TCTGAATCACCG 14206
                                                                                                                                                                                                                                                                                                                                                                                    AMACTIAGGAAGAACTICGAAGAGIGITIGAAATIAAAAGGGGTICCGGAAGATAACCTC 13789
                                                                                                                                                                                                                                                                                                                                                                                                                                       13849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13970 AACAAATTGCGGTGTTTCTGCGGTACTTTTCAGAAGGACTACATATCCTTGCGCAAGGAA 14029
                                              /procein_id="CAA51870.1"
/db_xref="G1:405633"
/db_xref="G1:405633"
/db_xref="SPTREMBL: Q08545"
/translation="WRFPLANGESFRALSRSESILRRVKELGTNSQGSEISBCVDEFN
ELASFNHLLVTVEHREWMEQHRNQSSKLRVPSRISEMIKEIRAFLKVRVVTPMHKETA
SDTLNAFLEGYCRITGLAREDALREKORRVKSVVLFHHSELLKFEVTENMFSYTELLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 05-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 ArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrPro 185
                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
                                                                                                                                                                                                                                                                                                                                                               LeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIle 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnArgAlaAspSerAspValIlePheSerAsnSerPhe---GlyGluArgAsnValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCysIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerTyrLeuAlaAlaPppeLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACTACTTAGCCGCTGACTTCATATCGACGTCGACGGAACTCACTGACCTACAAAGT
                                                                                                                                                                                                                                                                                                              SerAsnLeuSerAsnLeuVallleThrAspAlaSerSerLeuAsnGlyValAspLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                      13790 GGAATCGCGTTAGGACTTTGTTTGTATTCCTGTGCTACGATAGGCACTTCCAACAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 ValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaProLeuThrArgPheThr
                                                                                                                                                                                                                                                                                                                                                                                                              47 GluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCACTCACGGTGAATTGAATTCCTTTCTGGGGTCTCAAAAACTTTTGGAGGGAAAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                15480
71
29
87
2
                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIAACCAGITIGAAACAACIAGGICGI 14233
                                                                                                                                                  4463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 ValSerAsnleuArgGlnLeuGlyArg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     783 bp
Sequence 1 from Patent WO9428147.
A41914
                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                      US-09-613-486-15 (1-198) x BYVUAA (1-15480)
SGGELEILTFSKNEVILKRW"
                                                                                                                                                 3680 3
                                                                                                                         LNLSLRVISSOILGMAI"
          14768. .15301
/note="orf8"
/codon_start=1
                                                                                                                                     299. .15480
3446 c 368
                                                                                                                                                                                               9.23e-20
286.00
52.91%
37.57%
28.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A41914.1 GI:2297469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beet yellows virus
                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                   3891
                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106
                                                                                                                                                                                                                                                                                                                                                                27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A41914
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                  COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
             CDS
                                                                                                                                               BASE CO
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                င်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \delta
                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                    G
                                                                                                                                                                                                                                                                                                                                                                                                              ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                 ò
```

```
BYJ51931 10545 bp RNA linear VRL 05-APR-1999 elect yellow stunt virus helicase gene, partial cds; and RNA replicase, p30, p6, p66, p61, p25, coat protein, p18, and p22 genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 AAACTACGGAAGAATTTCGAAGAGTGTTTGAAATTGAAAGGGGTTCCGGAAGACAAACTC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 GGTCTCGCGTTAGAACTTTGTTTGTATTCCTGTGCGACGATAGGTACTTCTAATAAAGTT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 AACAAGTIGCGTIGITICIGCCGCACTITICAGAAGGACTACAIATCCTICGCGAAGGAA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 GluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 AsniysbeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCys1leAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 SerAsnLeuSerAsnLeuVallleThrAspAlaSerSerLeuAsnGlyValAspLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TyrLysHisLysLeuProGlmieuAsnAlaAlaAlaAlaGluLeuGlyIleProAlaGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgLysMetPheAlaSerMetTyrAlaLeulysThrGluGlyGlyValValAsnThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGTCTGCTGTTGGCGCGCGAAAACGCCACTCACACAGAGTTCTCG---TCTGAATCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 ValThrGluGlyAspleuLysLysValLeuAspGlyCysAlaProLeuThrArgPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 SerTyrLeuAlaAsaPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 LeuleuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGlylle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 GlnArgAlaAspSerAspValllePheSerAsnSerPhe---GlyGluArgAsnValVal
                                                                                                  PROTEIN GENES
  ANG OR
                                                                                                                                                                                                                                                                                                                                                                                                                   783
70
31
86
2
                                                                     Bojsen,K. and Brunstedt,J.

PAK, SSQUENCE COMPRISING AT LEAST TWO COAT

PARCET: WO 9428147-A 1 08-DEC-1994;

SANDOZ AG (AT)

Other publication AU 7122694 541220.

1. 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
Viruses, ssRNA positive-strand viruses,
Closteroviridae, Closterovirus.
1 (bases 1 to 783)
                                                                                                                                                                                                                                             /organism="Beet yellows virus"
/mol Lype="genomic DNA"
/db_xref="taxon:12161"
178 c 171 g 211 t
                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValSerAsnLeuArgGlnLeuGlyArg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-613-486-15 (1-198) x A41914 (1-783)
```

ORGANISM

KEYWORDS

VERSION SOURCE REFERENCE

ACCESSION

us-09-613-486-15.rge

```
/prodecin id="AAC55663.1"
/db_xref="G1:1388134"
/db_xref="G1:1388134"
/db_xref="G1:1388134"
/db_xref="G1:1388134"
/fcranslaterscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscriperscripersc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGSSSYLPGIKSILQSVDFVSECIDLPDPRAAVAAGCALYSSCLSSESPMILVDCASH
NLSIPNYVGESIVLVPAGAPVPFVOTRDINLASCVGSGSYSPVI-FEDDRTKCFYNKKV
SGSTVVRLADGCATGOTPRIINTVLATEPSSSVGTVFTITTGIASKKVFVVGGVPAVDFSK
ESVSIRSITELHTDNORNVILALTITKTRERAQKFSYSEKQHIDSILSGNIDTEKESKK
FNGYNEQTADVCRIILLGKSVQKTLRGARVEELSYRNIYEVQTIKI"
                                                                                          GFDPELLSVAMMEGEYRSERNTMDGOVGFTVDCQRKSGASNTWIGNSVVTLGILAMYYD
VSRYGALEVSOSDDSI.IRSADBIANYRABDIOLEJGFBTKFLTPSVPYFCSKFLVPTGDK
CVFVPDPYKLLVKLGASGRRI.SDELFEVFVSFRDI.TKEFGDGRVLATLSEI.VHIKYE
FEWGNYKLALSTIHCLRSNFLSPEKLFVKRTGWKVVYGKAKYILKKFLGYNIEPITTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSVLASTLPTLTSSVFEVQSNGEFLSLKRYRMNDERRRITTGAEMTIPHSDAKIFHVQ
VKQYDGNTGLLVYNGPHLILGGTIVRQFDILQGSCBNAYADLACPTSRFSFEVSDVL
CDCPMSFEIINTSDINNRSACTDAFYRRVVFEDSGGLLDTVDDSNSERHVSVDLRAES
SSRGDPRDVPLSSGEPEKASVLRNRNAMGLFLLVLLLAGATIYVYPNLSRFGVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAC55662.1"
| da xref="G11:138813"
| translation="WVPGVDFGTTFSSVCVFNSGRLHVFKQQNSAXIPTCLELYSDT
| mamspgydaetasldpnvkggfprdlkRmvgcdetnlebykgKlkPHYSVTLSNFGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRK.PTLGSYSGSVOMSGSLSGLIALFIQALVKSAAIEFKCECTELIVSVPANCDCMO
EFETBNCWINGSFTCWHMMEDSAAALSTGGRTMSAANLIVYDFGGGTFDVSVLSSL
NQTFVYRASGGDWNLGGRDVDRFKKKIYOMANLPFDERAD'SSKLSKIYPFTY
TVKTKDGESKTVVVSRGLLAEVIVPFVDRTIKVMKRVFELYVKNMNLKAQDAKASLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="ORF5; similar to analogously positioned proteins of other closteroviruses"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFPDELQKRVPDVSLRRRFNGAKAGEAITVFKKLGISFPPITRLNAPSKYSYLNIDYF
KQANSLGLTEPEKIILCNIAKDVDMMCAQRISSVKAKPIAQRNGEAINSAKIRT.:PTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MALYKYSALALIVDPDRRTYSFSFNLRAIFSACDARVFQGVSVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MDCILRAFLFFGFAIVICFFIAVAAYFFAFFVKNTHSQDTDVDI/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ORF6; similar to analogous BYSV coat proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ORF3; similar to small hydrophobic proteins of other closteroviruses"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to HSP70 homologs of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLVRALEKCLLNQAPSWWNTTLTNLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="p25"
/protein_id="AAC55664.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAC55660.1"
/db_xref="GI:1388131"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAC55661.1"
/db_xref="G1:1388132"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other closteroviruses"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="unknown"
/note="ORF4; similar '
closteroviruses"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4401. .4556
/function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5285. 7889
/function="unknown"
                                                                                                                                                                                                                                                                                                                          1522. .4343
function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="p61"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="p66"
                                                                                                                                                                                                                                                                                                                                                                                                                /note="ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .6409
                                                                                                                                                                                                                                                                               FGDAWFVYKE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /produčt="helicase"
/produčt="helicase"
/protein_id="AACS56.9.1."
/db_xref="G1:1381129"
/translation="SSFLCVVDWLRSQYCFISNKYFKSVGDSVYFKAVPTIINYKRRP
/translation="SSFLCWVDWLRSQYCFISNKYFKSVGDSVYFKAVPTIINYKRRP
/translation="SSFLCWYDWLRSQPSGPSWRSQPSGPSWRSQPSPSWRYPUNDSFRENGPSTRANFWNDVAGGIKIERAQRSGPSGPSWRTILDSFRKYTUQELTLFEIFNKLNRYFSELE
TLUSKFLNLWNTENAFPEPMIIEAHDLASNSVREFYYLQELTLFEIFNKLNRYFSELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHKKOR ILVLTANKSSQVEILKKINDSLKREHETKTKLLKFASKAERENYPSADSNYY
TIDSYLMYHLGTKCDYLFYDECFMYHAGAYDAYSNTLVPRSYFFYGDSRQIHHIERNE
YENASFSDLDBLVAAKDRIYGQVSYRCPMDVCGMLSKHYPNYATTNYESEGKSSLTI
TENYBYDYDASKRYTYLFFLEKELEKHLAKKGYRATVKTVHEAGGDTKTDYUL
RTKFQEDAPFSSFNHINVAITHHTESLIYAYLLAARRINNIAAALCEANELVDVYH
HSFGGSVLNIDVEPYTDNSRCKASSAPINSINDFLEDVYPGSTSLNFGDTSAEMESQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /produčt="RNA replicase"
/protein.id="AAC55659.2"
/bxctein.id="AAC55659.2"
/bxref="Gz:455941PKRRPSLQENLLSYEARNYNFITCERFSGFHEYGRA
/translation="SVVRSQAIPKRRPSLQENLLSYEARNYNFITCERFSGFHEYGRA
MAANVLKRCFPLDKVAAIRSDIIAITGRGFREWLSKRSPSQKKSLASDLETPLNLEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVEFDRKICRAGDDARLLVYRESDASLYGKDGRRPLKDMEFYEFVFRTGGLLPNDKEF
SGNKLFHANTKFIAANSFLRSNSSYRNFIFENDSCRIRLYEAPPGGGKTHTLIASFVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening of the closterovirus genome by degenerate primer-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ORF1b; similar to RdRp's of other closteroviruses;
the BYSV RdRp is presumably expressed via a +1 ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Characterization of the beet yellow stunt virus coat protein gene Phytopathology 88 (10), 1040-1045 (1998) 4 (bases I to 10545)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 10545)
Karasev, A.V., Nikolaeva, C.V., Lee, R.F., Wisler, G.C., Duffus, C.E.
and Dawson, W.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Organization of the 3'-terminal half of beet yellow stunt virus genome and implications for the evolution of closteroviruses Virology 221 (1:, 199-207 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (20-MAR-1996) Alexander V. Karasev, University of Floritd, Citrus Research and Education Center, 703 Experiment Station Road, Lake Alfred, F. 31850-2299, USA On Jun 25, 1996 this sequence version replaced gi:507953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 10545)
Karasev,A.V., Nikolaeva,O.V., Mushegian,A.R., Lee,R.F. and
Dawson,W.O.
                                                                                                                                                                                                                                                                                                                          : (bases 2734 to 5576)
Karasev, A.V., Nikolaeva, O.V., Koonin, E.V., Gumpf, D.J. and
                                                                                                                                                                                     Beet yellow stunt virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
Closteroviridae; Closterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ORFia; similar to helicases of other closteroviruses"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic_RNA"
/specific_host="Sonchus oleraceus L."
/db_xref="taxon:35290"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Beet yellow stunt virus#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymerase chain reaction

J. Gen. Virol. 75 (Pt 6), 1415-1422 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFESGANNVTVRDSAKPGSGTDHDEQRV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function="replication"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                          Beet yellow stunt virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coden_start=1
U51931 L20761
U51931.1 GI:1388128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .10545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                     Garnsey, S.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Karasev, A.V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94267425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96266429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8661428
```

source

FEATURES

COMMENT

CDS

CDS

PUBMED REFERENCE

AUTHORS

TITLE

JOURNAL MEDLINE

TITLE

MEDLINE PUBMED

JCURNAL

TITLE

REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS TITLE JOURNAL

```
Direct Submission

Submitted (12-APR-2002) Plant Pathology, University of Florida, 700

Experiment Station Road, CREC, Lake Alfred, FL 33850, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="coat protein"
/protein_id="AAM22216.1"
/db_xref="GI:CO454249"
/translation="MDDETKKLKOKRYKETKEGDDVVAAESSFGSMNLHIDPTLIAMND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VROLGTQQNAALNRDEFLTLKGKYPNLPDEDKOFH!AMMLYRLAVKSSSLQSDDDTTG
ITYTREGVEVDLSDKLMTDVVFNSKGIGNRTNALRVMGRTNDALYLAFCRQNRNLSYG
GRPLDAGIPAGYHYLCADFLTGAGLTDLECAVYIQAKEQLLKKRGADEVVVTNVRQLG
3884 AAGACACCGTTAGTGAGCGCTAAGATAGATGCGGTCAACGTGACGATAACTTAAGAAGAC 8943
                                                                                                                                                                                                                                9064 CCGAATATCGCAAGAGGGAACAAACACGGTATTCCCCGCTGATTACTCGTATTTAGCAGCT 9123
                                                                                                                                                                                                                                                                                                            9124 GACTTCGTCCAAACTAGCAACTTATTGAAAGAGCACGAACAGGCA---GTACTTCTGGAA 9180
                                                                                                                                                                                                                                                                                                                                                                                            9181 GGTAGAAACGCTGCTACAGCATCTTCCGGCACCACTAGGGAGTCTGCGGTCAACCTAAAA 9240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRL 02-APR-2003
                                     LeuLyslysulLeuAspGlyCysAlaProLeuThrArgPheThrAsnLysleuArgThr 110
                                                                                                                                                                                             150
                                                                                                                                                                                                                                                                         AspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGinSerArgLysMetPheAla 170
                                                                                                                 111 PheGlyArgThrPheThrGluAlaTyrValAspPheCysIleAlaTyrLysHisLysLeu 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roy, A., Ramachandran, P. and Brlansky, R.H. Grouping and comparison of Indian citrus tristeza virus isolates based on coat protein gene sequences and restriction analysis
                                                                                                                                         131 ProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAspSerTyrLeuAlaAla
                                                                            8944 ATTAAGAACTTGGTAAACTCCTTGACGTTGCTTAAGAACTATAAGAATAAACTCCGAGTG
                                                                                                                                                                                                                                                                                                                                                   171 SerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrProValSerAsnLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          672 bp RNA linear VF
Citrus tristeza virus coat protein gene, complete cds.
AF501867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Citrus tristeza virus
Viruses; BSRNA positive-strand viruses, no DNA stage;
Closteroviridae; Closterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     672
61
27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Citrus tristeza virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'country="India: Bangalore"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arch. Virol. 148 (4), 707-722 (2003)
22548851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic RNA"
/db_xref="taxon:12162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF501867.1 GI:20454248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Citrus tristeza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.71e-05
130.50
40.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 672)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9241 TATCTTGGG 9249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .672
                                                                                                                                                                                                                                                                                                                                                                                                                                 191 GlnLeuGly 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12664295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                        9004
                                                                                                                                                                                                                                                                         151
                                  91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
ACCESSION
VERSION
KEYWCRDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF501867
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                 qc
                                                                                                             õ
                                                                                                                                           qC
                                                                                                                                                                                 ò
                                                                                                                                                                                                                            50
                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                  G
                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                      D.D.
                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CB
                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MKLLLSDSYYDSINLANKCLNELNNKSVPLESCIASYNELIK
VMAGSGSDAIRKNEKNENLFPLSVWTTDLELMVRDIRÇLIRAEINKEFNCSSNQDVV
VRIIRNVITHPSNSRERPVTFEQIOSFSMRGVIKTSLQNLSYKYKFEVTINYFKCNA
LLDVKMGVSVKTFVENYLGENLESFL"
              /translation="MPPOPGAELVEHNANKSSLEVPSSETREKVGKFFNNFDHKTFKQ
VPWILLNEDELREVLGHKTEHKWIKALLDEDTHWARFLELRASVVSYSFBYVBYKGS
YSYSIDQRKYTWNDAKIFPOYKILASYGHNKNGIRASCASLEGMYLLSYARLGPDAFGT
RSVGKRGAPSGSSYLGADFLISTCPLMSDHDRAVALSASRNALDBRSAASQIDKKVVSL
                                                                                                                                                                                                                                                                                                                               /trānslation="WAGGNDEGSDDSSASQTWTAKDWIFAPFENFARASATCLNGENX
KAFERENSWYKTQDVTESSGIPTLLGWTLYALATSSSSKIDIEDKFPPVSAKIDAW
VTITYEDIKKPWITLLKWYKWKLRYFARTFEEEVLAFVRQYKHIENIARAKHGI
PADYSYLAADFVQTSNILKEHEQAVLLEGRNAATASSGTTRESAVNLKYJGGSSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAVIESLQFVTPVHEKYALVLVTDQDAF1FEHLGVQHSSPYPVL
WYHGEGAMADGSVISFTYKELQDVLNSLLQYRTRMLRVRKTTSSSLELINVRATNAVV
SIFRCNAPTLIFVTSKGPEESMDAVLYNGIIGTPSVDPTHLLSSIVESYGNITHFAIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8704 AATTICGCTCGCGCGCGCGCGACTIGITICAAIGGIGAAAACAAGAAGIIGIICGAG 8763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8764 GAATTTTCTGTGAGAGTGAAGACTCAGGATGTCACTGAATCCGGCATTCCCACAACTTTG 8823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnLeuVallleThrAspAlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAla 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "note="ORF9; similar to the 20-kDa protein of CTV and the 21-kDa protein of BYV, two other closteroviruses"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyLeuLeuLeuTyrAlaLeuAlaArgThrThrSerProLysValGlnArgAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8617. .9264
/note="CP; CRF7; similar to coat proteins of other
closteroviruses"
                                                                                                                   /note="transcription start site for coat protein subgenomic RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to 3' UTR's of CTV and BYV"
2196 c 2497 g 2863 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10545
66
22
94
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein_id="AAC55666.1"
db_xref="GI:1388137"
                                                                                                                                                                                                                                                                                         /protein_id="AAC55665.1"
/db_xref="GI:1388136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAC55667.1"
/db_xref="G1:1388138"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1-10545)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                         product="coat protein"
                                                                                                                                                                                                                                                    evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                           9261. .9743
/function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
product="p18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        x BYU51931
                                                                                                                                                                                                                                  codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="p22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9746. .10306
                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="ORF8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266.50
48.09%
36.07%
26.89%
                                                                                            YDFGKVVYT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-613-486-15 (1-198)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
Score:
Percent Similarity:
Percent Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ಹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2989
                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                        SCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
```

ò g ें CD 8 q ò

-613-436	US-09-613-486-15 (1-198)	14 8) × AF501867	Gaps: (1-672)	11		
1 91	MetGluLer 	uMetSerAspSer/ 	1 MetGluLeuMetSerAspSerAsmLeuSerAsmLeuVallleTürAspAlaSerSerLeu 20		SerSerLeu 2 GTCAGTTG 3	20
21	AsnGlyva.	lAspLysLysLeuI	21 AsnGlyValAspLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGly	uLysMetLeuValC	slnitysgly '	40
145	GGAACCCA	ACAGAACGCCGCT1	TTGAACAGAGATTTG	TTTCTTACT(TGARAGGG	198
41 199	AAGTATCC	AlaProAsnC TAACTTGCCTGACC	41AlaProAshG.uGLylleGluValValPheGlybeuLeuLeuleulyrAla 	PheGlyLeuLeur 		25 55 25 8
, u		aArgThrThrSer-				63
V 0 4	11460661	i HAGAGI I CAT CGI	116chhholonionion	ראר הארפפפטראו אי	. IJW.ALI	0 7 0
319	CGGGAGGG	-ProLysvaigink ::: TGTTGAAGTGGAT1	64ProlygvalGinArgAtaAspSerssyalilePheSer 	-SerAspvalllei :::' '::: GACTGACGTCGTG		76 373
77	AsnSerPh	eGlyGluArgAsnV	77 AsnSerPheGlyGlwArgAsnValValValValThrGluGlyAspLeuLysLysValLeuAsp	yAspleulysLys	valLeuAsp	96
379	AAGGGTAT	TGGTAACCGT				396
9.7	GlyCysal	aProleuThrArga	GlyCysAlaProJeuThrArgPheThrAsnLySLeuArgThrPheGlyArgThrPheThr	gThrPheGlyArg		9
397			ACTAATGCCCTTCG	 		432
117	7 Glualary	rValAspPheCys	117 GlualaryrValAspPheCyslleAlaTyrLysHisLysLeuProGlnLeuAsnAlaAia 136	sLeuProGlnLeu	AsnAlaAia	136
433	GCCCTTTA'	TTTAGCTTTCTGT.	AGACAGAATCGCAA	TTTGAGTTATGGT	3GACGTCCG	489
137	7 AlaGluLe	uGlylleProAlac	137 AlaGlubeuGlyIleProAlaGluAspSerTyrbeuAlaAlaAspPhebeuGlyThrCys 156	aAlaAspPheLeu(SlyThrCys	156
490	CTAGATGC	AGGGATICCGGCT	GGATATCATTACCTATG	TGCAGATTICTIG	ACCGGA	246
157	7 ProLysie	uSerGluLeuGlad	157 ProLysLeuSerGluleuGlmGlmSerArgLysMetPheAlaSerMetTyrAlaLeuLys 176	eAlaSerMetTyr;	AlaLeuLys	176
547	GCIGGCII	 GACTGATTTAGAA1	TGTGCTGTGTACATACA	AGCTAAGGAACAA	TGTTGAAG	909
177	ThrGlug]	yGiyvalv	177 ThrGluGlyGlyValValAsnThrProValSerAsnLeuArgGlnLeuGlyArg	rAsnLeuArgGln]		194
637	AAGCGAGG	GGCTGATGAAGTCC	.: GTAGTTAC	TAATGTCAGGCAG		657

Search completed: November 8, 2003, 00:59:54 Job time : 3533 secs

Run on:

```
7, 2003, 23:40:55; Search time 267 Seconds (without alignments) 2001.830 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_192un03:*

1. /S1D51/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
2. /S1D51/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3. /S1D51/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4. /S1D51/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5. /S1D51/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
6. /S1D51/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7. /S1D51/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
8. /S1D51/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
9. /S1D51/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
9. /S1D51/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2010.DAT:
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2010B.DAT
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | SIDS://goddara/geneseq/geneseqn-embl/NA1994.DAT.
| SIDS://goddara/geneseq/geneseqn-embl/NA1994.DAT.
| SIDS://gogdara/geneseq/geneseqn-embl/NA1995.DAT.
| SIDS!/gogdata/geneseq/geneseqn-embl/NA1995.DAT.
| SIDS!/gogdata/geneseq/geneseqn-embl/NA1996.DAT.
| SIDS!/gogdata/geneseq/geneseqn-embl/NA1997.DAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS1/gcgdata/geneseq/genesegn-emb1/NA2303.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS1/gcgdata/geneseq/geneseqn-emb]/NA1989.DAT:
/SIDS1/gcgdata/geneseq/geneseqn-emb]/NA1990.DAT:
/SIDS1/gcgdata/geneseq/geneseqn-emb]/NA1991.DAT:
                                                                                                                                                                                                                                                                                                1 MELMSDSNLSNLVITDASS1......GGVVNTPVSNLRQLGRREVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5105512
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                  frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2552756 seqs, 1349719017 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                 Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                     using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 200000000
                                                                                                                                                                                                                                                 US-09-613-486-15
                                                                                                     - nucleic search,
                                                                                                                                                    November
                                                                                                                                                                                                                                                                                                                                               BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vinimum DB :
Maximum DB :
                                                                                                  OW protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
```

```
and is derived by analysis of the total score distribution
```

ห ชื่อ เ	sult No.	34 I G	n a contra	Length	2B 	⊴ '!	scription
	,,,	991	0.001	597	20	AAV08870	Sevine 1
	1 17	nσο	28.	ם ר	9 71	53	+ 3-
	4	28	ω.	-	9	175	BYV coat protein c
	un va	· α		ഗെ	24	3.9	C. albicans BAX-as arabidonsis thalia
	٠,	98		12	2:1	12	Arabidopsis thalia
	ထင	10 a	8.7	349980	22	31	Pyrococcus abyssi
	10	٠.		* [55	65	GLRaV-5 rucleotide
υ	11	83.5		9	24	187	Buchnera sp. genom
	25			\sim	לי נ	13	Srysipelothrix rhu
	1 m			\circ	21	87.	Erysipelothrix thu
	15	; ;		œ	21	17	Erysipelothrix rhu
t)	76	Ë.		0	20	148	Borrelia burgdorfe
D	r c	81	•	499	4, 0	149	Bitidobacterium lo
	0 0	· α	•	3 5	2 4	25	Streptocooring poly
	20	၁၈		4	24	03	Streptococcus poly
	2.5	30		in		1521	Genomic sequence o
	22	6.		Ξ.	23	18.7	Enterococcus faeca
	23	7.9		47 L	3 6	27.	Grapevine leafrol:
	4 ر ب	y 6	•	ηα	3 5	3.6	Orosophila melanog
	26	9,6		, ,	253	0 50	Enterococcus faeca
	27	79		· m	24	154	Enterococcus faeca
	28	66	•	6	21	00	Grapevine leafroll
U	0,0	ر. و د	•	613	2 2		Propionibacterium
) . I	97			9 4	62	Rhizobium species
	32	œ,	•	22	22	170	C.
	33	77.5		Ψ.	54	691	
	9 r	۲. ر	•	4 C	23	146	Drosophila melanog
	ን ሳ ያ			917	7 7	003	٠,
	o t^	77		$^{\circ}$	24	22:	1
	38	S		7676	σ. • •	908	ಡ
	9	76.5		C	24	130	1)
O	40	96		009	22	104	Ð
υ	7.	76		009	55	98	9
U	4, 4	9 6		200	77	74.7	ov :
U I	2. d	2 (•	9 0	7 6	27.0	Fuch #7406 for an
υυ	4 4 0	9 6		000	22	/3 82	Probe #11068 used
						ALIGNMENTS	
RES	SULT 1						
AAVO	3870						
G \$	AAV	s 01880.	tandard	d; conh;	597	1 ВР.	
A S	AAV	V08870;					
×							
TC	9	MAR-199	9 (fi	rst entr	. ,		
E E	Gra	pevine	leafrol	11 virus	typ.	e 2 coat protein ORF6 p	roduct.
X ž š	1	aV-2;	icst	virus;	gra	e; tobacco; transgenic p	lant;
*	tri	ease re steza v	7 H	ce; viru coat pro	is re otein	sistance; beet yellows v ; ss.	T.T.
so:	Gra	apevine	leafro	ll virus	typ.	De 2.	
Y Z	860M	53055-	A				
:	2	1	ς .				

≎

```
3) CICACTAGGITCACTAAIAAACIIAGAACGITOGGICGIACTIICACTGAGGCIIACGIT 360
                                                                                                                             480
                                                                                                                                                          161 GlubeuGlnGinSerArgiysMetPheAlaSerMetTyrAlaLeuiysThrGluGlyGly 180
                                                                                                                                                                                            540
                                                                                               141 IlePrcAlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer
                                                                                                              ATTCCAGCTGAAGATTCGTACTTAGCTGCAGATTTTCTGGGTACTTGCCCGAAGCTCTCT
                                                                                                                                                                              481 GAATTACASCAAAGTAGGAAGATGTTCGCGAGTATGTACGTCTAAAAACTGAAGGTGGA
                                                                                                                                                                                                                           ValvalAsmIhrProValSerAsmLeuArgGinLeuGlyArgArgGluValMet 198
                                                                                                                                                                                                                                             /product= polyprotein (protease, methyltransferase,
helicase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRLaV-2; closterovirus; grape; tobacco; transgenic plant; disease resistance; virus resistance; beet yellows virus; tristeza virus; protease; methyltransferase; helicase; heat shock protein; coat protein; RNA polymerase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= b
product= RNA-dependent RNA polymerase
note= "Claim 29"
                                                                                                                                                                                                                                                                                                                                                                                                                         Grapevine leafroll virus type 2 (GRLaV-2) genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product= heat shock 70 protein
note= "Claim 32"
1277..12932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product= diverged coat protein
note= "Claim 41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= hydrophobic protein
/note= "Claim 43"
9551..11350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= coat protein
fnote= "Claim 38"
4180..14665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                undefined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product= undefined
                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Claim 45"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Claim 26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Claim 35"
2844..13515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Claim 47"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grapevine leafroll virus type 2.
                                                                                                                                                                                                                                                                                                                           AAV08874 standard; cDNA; 15500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3584..14180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .4667..15284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   922..9301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9365..9535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag= e
product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                '*tag= g
'product='
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag=
                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-1999
                                                                                                                                                                                                                            181
                                                                                                                             421
                                                                                                                                                                                                                                                                                                         Ω,
                                                                                         8 8
                                                                                                                                                  ें
                                                                                                                                                                                     G
                                                                                                                                                                                                                           ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AATGGTGTCGACAAGAAGCTTTTATCTGCTGAAGTTGAAAAATGTTGGTGCAGAAAGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuThrargPheThrasnLysLeuArgThrPheGlyargThrPhethrGlualaTyzVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGly 80
                                                                                                                                                                                                                                                                                                                   This is the nucleotide sequence of open reading frame ORF6 of grapevine leafroll virus type 2 (GRBAV-2) RNA (see AAV08874). It codes for a 22 kDa coat protein (see AAV08864-72; for a genome includes 9 open reading frames (see AAV08864-72; for a polyprotein, an RNA-dependent RNA polymerase, heat shock proteins, coat proteins and proteins of unknown function (see AAW13476-84). These can be used to produce antibodies useful for detecting GLRAV in samples e.g. by ELISA (claimed). The nucleic acid molecules can be used to produce probes and primers for such detection, and to transform host cells (especially Agrobacterium vitis, Agrobacterium tumefaciens, grape, citrus, beet or tobacco vitis, Agrobacterium tumefaciens, grape, citrus, beet or tobacco colingart GLRAV-2 resistance to Vitis schon or rootstock cultivars or impart GLRAV-2 resistance to Vitis schon or rootstock cultivars cloimed). Because extensive similarity exists between hspor-relaced sequence regions of GLRAV-2 and other closeroviruses, the ENA may also be used to impart beet yellows vitus resistance to beet cultivars or tristeza vitus resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 AsnGlyValAspLysJysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysJly
                                                                                                                                                                                                                                            Ç
                                                                                                                                                                                                                       Grapevine leafroll virus (type 2) proteins and polypeptides - and encoding DNA, useful e.g. to impart grapevine leafroll resistance grape and tobacco plants and detect grapevine leafroll virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
00
00
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 597 BP; 165 A; 121 C; 157 G; 154 T; 3 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    citrus scion cultivar/rootstock cultivars (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-09-613-486-15 (1-198) x AAV08870 (1-597)
                                                                                                                                                                                                                                                                                         Claim 38; Page 44; 151pp; English
                                                                                                          (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.15e-117
991.00
10c.00%
1co.00%
                                               98WC-JS10313.
                                                                              97US-0047194.
                                                                                                                                           Gonsalves D, Ling K,
                                                                                                                                                                           WPI; 1999-045307/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ercent Similarity:
Best Local Similarity:
                                                                                                                                                                                         P-PSDB; AAW73482
                                             20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lignment Scores:
               26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  red. No.:
```

score:

g à 5

à

9

ਨੇ

q

ਨੇ

à

3'UTR

13823

100

13883

13943

120

14003

160

140

14123

180

```
The nucleotide sequence of the novel gene encoding the sugar beet yellows virus (SBYV) capsid protein. The gene encodes a protein of 204 amino acids with mol. wt. 22.2 kD. The gene was obtained from reverse
                                                            13764 ACCACGTCTCAPAGGTTCAGCGCGCAGATTCAGACGTTATATTTTCAAATAGTTCGGA
                                                                                                              GluArgAsnValValValThrGluGlyAspieuLysValLeuAspGlyCysAiaFro
                                                                                                                                                                                                                                         14. IleProAlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14064 GAATTACAGCAAAGTAGGAAGATGTTCGCGAGTATGTACGTCCTAAAAACTGAAGGTGGA
                            61 ThrThrSerProLysValGlnArgAlaAspSerAspValilePheSerAsnSerPheGly
                                                                                                                                                            13824 GAGAGGAATGTGGTAGTAACAGAGGGTGACCTTAAGAAGGTACTCGACGGGTGTGCGCCT
                                                                                                                                                                                                                                                                                                     121 ASPPHECYSILEAlaTyr_ySHisLySLeuProGlnLeuAsnAlaAlaAlaGluLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluLeuGlnGlnSerArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGly
                                                                                                                                                                                                            1C1 LeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ValValAsnThrProValSerAsnLeuArgGlnLeuGlyArgArgGluValMet 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product = sugar beet yellows virus capsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugar beet yellows virus cDNA fragment encoding capsid protein useful for production of virus-resistant transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugar beet yellows virus capsid protein; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugar beet yellows virus capsid protein coding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Karasev AV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Column 7-10; 5pp; Russian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   뎚
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BICYRCHN INST CO LTD. IMMUNOBIOTECHN INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ87853 standard; cDNA; 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91SU-4950054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91SU-4950054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Argancvskii AA, Boiko VP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beet yellows virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74..688
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-113715/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR72682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RU2017820-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
02-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ87853;
                                                                                                                   . 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOT=)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMI)=)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC87853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC
                                                                                                                                                                                                                                                ਨੂ
                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                     දි
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13644 AATGGTGGACAAGAAGCTTTTATCTGCTGAAGTTGAAAAAGTTGGTGCAGAAAGG 13703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type 2 (GLRAV-2) has been sequenced and cloned from GLRAV-2 isolated from infected Vitis vinifera ov. Pinot Noir. About 83% colorated from infected Vitis vinifera ov. Pinot Noir. About 83% cof the total RNA genome was revelaed from 2 different clones. The sequence in the coat protein gene region was determined and confirmed from several overlapping clones. The sequence in the coat protein gene region was determined and corpulation of GLTAV-2 includes 9 open reading frames (see also AAV08864-72) encoding a polyprotein (see AAW71476) having papain-like proteinse, methyltransferase and helicase motifs, an RNA dependent proteins of unknown function (see AAW71476-84). These proteins can be used to produce antibodies, useful to detect GLRAV in samples e.g. by ELISA (claimed). The nucleic acid molecules can be used to produce probes and primers for such detection, and to transform host cells (especially Agrobacterium vitis, Agrobacterium fortuna cells (especially Agrobacterium vitis, Agrobacterium tumefactens, graph cittus, beet or tobacco cells) and produce impart GLRAV-2 resistance to vitis scion or rootstock cultivars or impart GLRAV-2 resistance resinant beet yellows virus resistance to cittus scion children to but way also be used to liminate beet yellows virus resistance to cittus scion colored to but this action or rootstock colored to but the but may also be used to liminate the colored to impart elected to impart sesistance to cittus scion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 AlabroAsnGluGlylleGluValValPheGlyLeuLeuLeuTyrAlaLeuAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 AsnGlyValAspLySLySLeuLeuSerAlaGluValGluLySMetLeuValGlnLySGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetGluLeuMetSerAspSerAsnLeuSerAsnLeuValIleThrAspAlaSerSerLeu
                                                                                                                                                                                                                                                                                                                                                                                            AAW73478, AAW73479, AAW73480, AAW73481,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grapevine leafroll virus (type 2) proteins and polypeptides - and encoding DNA, useful e.g. to impart grapevine leafroll resistance grape and tobacco plants and detect grapevine leafroll virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15500 BP; 3984 A; 3178 C; 3970 G; 4368 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-613-486-15 (1-198) x AAV38874 (1-15500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 12-20; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cultivar/rootstock cultivars (claimed)
                        /*tag= j
/note= "Claim 48"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.13e-115
991.00
100.00%
100.00%
                                                                                                                                                                                                                                                                           (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                       r-bsub; Aaw73476, Aaw73477, A
Aaw73482, Aaw73483, Aaw73484.
                                                                                                                                                                                                                                                                                                                           Zhu H;
.5285..15500
                                                                                                                                                                                                                                97US-0047194.
                                                                                                                                                                                    98WO-US10313.
                                                                                                                                                                                                                                                                                                                         Gonsalves D, Ling K,
                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-045307/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                20-MAY-1997;
                                                                                           WO9853055-A1
                                                                                                                                                                                    20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                      26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
```

ò g D, ò

ò

```
86 ValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaProLeuThrArgPheThr 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 SerAsnieuSerAsnLeuVallieThrAspAlaSerSerieuAsnGlyValAspiysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 AAACTACGGAAGAATTTCGAAGAGTGTTTGAAATTGAAAGGGGTTCCGGAAGACAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 GCGACTTTTGAAAACGTGAGTCTCGCAGACCAAACGTGTTTGCACGGTGAAGACTGCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 LeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 GGTCTCGCGTTAGAACTTTGTTTGTATTCCTGTGCGACGATAGGTACTTCTAATAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 GluValValPheGlyLeuLeuLeuTyrAlaleuAlaAlaArgThrThrSerProLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GinArgAlaAspSerAspValIlePheSerAsnSerPhe---GlyGluArgAsnValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAT42975-77 represent cDNA sequences encoding coat proteins from beet yellow virus (BYV) beet western yellow virus (BNYV) and beet necrotic yellow vein virus (BNYVV) respectively. These sequences are used in the recombinant DNA sequence of the invention. This comprises nucleotide sequences encoding the coat proteins of at least one luteovirus and at least one closterovirus. This recombinant DNA may be used to transform sugar beet for combatting viral infection. Other plants may also be transformed e.g. fruit such as mangoes, apples, pears, bananas, and field crops such as sunflower, wheat, barley, maize, and vegetables such as potatoes, carrots, cabbage and onion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant DNA sequence comprising at least two coat protein genes - used to combat viruses in e.g. sugar beet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 783 BP, 223 A, 178 C, 171 G, 211 T, 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                783
70
31
86
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
                                                                                                   sequence from TMV'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches:
Indels:
                                                                                                                                  /*tag= b
/product= BYV_coat_protein
                                                                                                                                                                                                                                                                                                                (SANO ) SANDOZ LTD.
(SANO ) SANDOZ PATENT GMBH.
(SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-613-486-15 (1-198) x AAT42975 (1-783)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 11-12, 23pp; English
                                                       Location/Qualifiers
                                                                                  a
"Omega s
                                                                                                                                                                                                                                                    94WO-EP01786
                                                                                                                                                                                                                                                                                     93GB-0011332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.6e-26
285.00
53.44%
37.04%
28.76%
                                                                                                   /note= "(
89..703
                                                                      13..78
                                                                                                                                                                                                                                                                                                                                                                                     Bojsen K, Brunstedt J;
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-022818/03.
                    Beet yellow virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                   02-JUN-1993;
                                                                                                                                                                                    WO9428147-A1
                                                                                                                                                                                                                                                    01-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                     08-DEC-1994
                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
O
                                                                                                                      CDS
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValThrGluGlyAspLeunysLysValLeuAspGlyCysAlaProLeuThrArgPheThr 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :::||| |||:::||| |||34 CTCACTCAGGGGTCTCAAAACTTTTGGAGGGAAAACCT 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerTyrLeuAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrPro 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               584 CGTCTGCTGTTAGCGCGGAAACGCCACTCACACGGAATTCTCG---TCTGAATCACCG 640
                                                                                                                                                                                                                                                                                                                      164 AAACTTAGGAAGAACTTCGAAGAGTGTTTGAAATTAAAAGGGGTTCCGGAAGATAACCTC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 AACGICCAACCGACGICTACCIICAICAAAGCIITGGIIGGGGGGGGAAGGAACIGIAC 343
                                                                                                                                                                                                                                                                                                                                                                    4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 GlnArgAlaAspSerAspValIlePheSerAsnSerPhe---GlyGluArgAsnValVal 85
     The fragment is useful for
                                                                                                                                                                                                                                                                                               SerAsnieuSerAsnieuVallieThrAspAlaSerSerieuAsnGlyValAspiysLys
                                                                                                                                                                                                                                                                                                                                                                    ieuLeuSerAlaGluValGluiysMetLeuValGlnLysGlyAlaProAsnGluGiyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                    47 GluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsniysLeuArgThrPheGiyArgThrPheThrGluAlaTyrValAspPheCysIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrLysHisLysLeuProGlnLeuAsnAlaAlaGluLeuGlyIleProAlaGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACCGAGGGAAATTACCTCCGATTGCCAGGCTAACCGTCACGGTCTACCCGCTGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tobacco mosaic virus; coat protein; beet yellow virus; BVV; beet western yellow virus; BWYV; beet necrotic yellow vein virus; BNYVV; luteovirus; closterovirus; sugar beet; fruit; mango; apple; pear; banana; field crop; sunflower; wheat; barley; maize; vegetable;
transcribed RNA isolated from purified SBYV. The fragment is the production of virus resistant transgenic plants by genetic engineering methods.
(Updated on 25-MAR-2003 to correct PN field.)
(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                     other;
                                                                                                                                                    688
777
229
229
229
                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                  Sequence 688 5P; 190 A; 155 C; 157 G; 186 T; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValSerAsnLeuArgGlnLeuGlyArg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAACCAGTTTGAACAACTAGGTCGT 667
                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                    US-09-613-486-15 (1-198) x AAQ87853 (1-688)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  potato; carrot; cabbage; onion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                  9.9e-27
286.00
52.91%
37.57%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                  28.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT42975 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BYV coat protein cDNA.
                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JAN-1997
                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                    27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT42975
                                                                                                                                                                                                                     Query Match:
                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT42975
                                                                                                                                                                       Score:
                                                                                                                                                                                                                                   DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
     888888888
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΩΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

99

85

```
SerTyrieuAlaAlaAspPheieuGlyThrCysProLysLeuSerGluLeuGlnGlnSer 165
                                                                                                                                                                                                                                                           185
CTCACTCACGGTGAACTGAGGTCTTTTCTGGACTCTCAGAAACTTTTGGAAAGGAAAGCCT 418
                                    AsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCysIleAla 125
                                                                                                                                     539 CACTACTTAGCTGCTGATTTCATATCGACATCAACAGAACTTACTGACCTACAACAAGGT 598
                                                                                                                                                                                                                                                                                Bax gene. The Bax gene of the invention is useful for identifying Bax-resistant yeast or fungi, identifying, or obtaining and identifying Candida app. sequences that are differentially expressed in a pathway eventually leading to programmed cell death or identifying inhibitors of inhibitor sequences of Bax-induced cell death. The products of the invention have exposeratic, fungicale; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The isolated nucleic acids, polypeptides, pharmaceutical compositions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bax, Bax-resistance, cytostatic; fungicide, immunosuppressive, virucide, vasotropic, vaccine; gene therapy, proliferative discreer, cancer, apoptosis, fungal, yeast, infection; autoimmune disease; ischaemia; neurodegeneration; cell death, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid representing a synthetic Bax gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in certain diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel nucleic acid representing a synthetic
                                                             TyrlysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAsp
                                                                                                                                                                                                                                                           ArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reekmans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fragment SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luyten WHML,
                                                                                                                                                                                                                                                                                                                             ValSerAsnLeuArgGlnLeuGlyArg
                                                                                                                                                                                                                                                                                                                                                      Claim 36; Figure 2; 344pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. albicans BAX-associated cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ76539 standard; cDNA; 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-2000; 2000EP-0870318.
04-JAN-2001; 2001EP-0870002.
09-JAN-2001; 2001EP-0870003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eberhardt 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-2001; 2001WO-EP15398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-667002/71.
P-PSDB; ABG93273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W0200264766-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contreras RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-NCV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2002
 359
                                                                                                                                                 479
                                                                                                                                                                                   146
                                                                                                                                                                                                                                                                                                599
                                                                                                                                                                                                                                                                                                                                                                     959
                                                                         419
                                                                                                            126
                                                                                                                                                                                                                                                           166
                                                                                                                                                                                                                                                                                                                                  186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB076539;
                                    106
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                               ABQ76539
                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cp.
                                                                                                                                                                                 ò
                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                  ò
g
                                    ò
                                                                                                            ਨੇ
                                                                                                                                         QC
QC
```

```
preparing a medicament for treating, preventing and/or alleviating diseases associated with yeast or fungi or proliferative disorders, such as cancer, or for preventing apoptosis in certain diseases. The compounds or polypeptides, or the genetically modified organism are useful for preparing a medicament for modifying the endogenic flora of humans and other mammals. The vaccine is useful for immunising against yeast or fungal infections. Apoptosis-related diseases include autoimmune disease, its chemia, diseases related with viral infections or neurodegenerations. This sequence represents a polynuchectide associated with the Bax gene described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glu------LeuGlyIlePro---AlaGluAspSerTyrLeuAlaAlaAspPheLeu 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 GlyThrCysProLysLeuSerGluLeuGlnGlnSerArgLysMetPheAlaSerMetTyr 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          517 Troatdocricinggaaatroggaccagricingcractogriciaccactgringaag 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuMetSerAspSerAsnLeuSerAsnLeuVallleThrAspAlaSerSer --- LeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 745 ACCEGIAAAATIATCAIGAAAIIGGCIGCIGAAICAAACIIGAAAAAAGIIACITIGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4: AlaProAsnGluG_yIleGluValValPheGlyLeuLeuLeuTyrAlaLeuAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGGGTGGTAAATCTCCAAACATTGTTTTCAACGAT-----GCTGATTTGGACAAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       859 ATTCAAAACTTGATTGTTTCTATCTTCTACAATTCTGGTGAAGTCTGTTGTGCTGGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TyrLysHisLysLeuProGlnLeuAsnAlaAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               919 CGTCTTTTGATTCAATCCGGTGTTTACGACCAAGTTGTTGAAAAATTCAAAGAAGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            637 ATGCCAAAAGSTGTTATCAACATTGTTTCTGGTTTTTGGTGCTACTGCTGSTGCTGCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrInrSerProlysValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      697 GCTAAACATCCAAAGATTGAAAAA------GTTGCTTTCACTGGTTCTACTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuAspGlyCysAlaProleuThrArgPheThrAsnLysLeuArgThrPheGlyArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AspPheCysIleAla----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyValAspLysiysLeufeuSerAla---GluValGluLysMetLeuValGlnLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  577 ACTGCTGAATCCACCCATTATCTGCTTTATATCTTTCCCAATTGTTAGTCGAAGCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluArgAsnValValVal -----ThrGluGlyAspLeuLysJysVal -----
antisense molecules and antibodies are useful as medicaments or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||-||
| GADAGGGCTAAGGTAGGTAACCCATTCGACGAAGACACTTTTATGGGTGCC-
                                                                                                                                                                                                                         Sequence 1500 BP; 442 A; 291 C; 309 G; 458 T; 0 other;
                                                                                                                                                                                                                                                                                 1500
33
39
76
12
                                                                                                                                                                                                                                                                                                                     Conservative:
Xismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::: |||::::::|||
TCTGGTAAATCTCAAGGTGCTACTGTTTACC 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 AlaLeuLysThrGluGlyGlyValValAsnThr 184
                                                                                                                                                                                                                                                                                   Length:
Xatches:
                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                  x ABQ76539 (1-1500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheThrGluAlaTyrVal------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC45964 standard; DNA; 1197
                                                                                                                                                                                                                                                                                                 89.50
43.60%
25.12%
9.03%
                                                                                                                                                                                                                                                                                   .387
                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-613-486-15 (1-198)
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        رب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC45964
                                                                                                                                                                                                                                                                                                                                                               Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC45964
ID AAC
XX
AC AAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                Arabidopsis thaliana DNA fragment SEQ ID NO: 48418
                                                                                                                                                                                                                                                                                                                                                                                     990S - 012182S - 990S - 012182S - 990S - 012548 - 990S - 013248 - 990S - 013455 - 990S - 013455 - 990S - 013455 - 990S - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013945 - 013
                                                                                                                                                                                                                                                                                                                                             2000EP-0301439
(first entry)
                                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1999;
28-APR-2999;
30-APR-1999;
30-APR-1999;
64-MAY-1999;
05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 - 70N - 1999)
                                                                                                                                                                                                                                                                                                                                          25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUN-1999;
16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
                                                                                                                                                                                                                                               EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -MAY-1999;
-MAY-1999;
-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -MAY-1999;
-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -MAY-1999;
-MAY-1999;
-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -MAY-1999;
-MAY-1999;
-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -MAY-1999;
-MAY-1999;
-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -JUN-1999;
18-OCT-2000
                                                                                                                                                                                                                                                                                            06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUN-1999
```

```
PR 28-JUN-1999 99US-0139750
PR 21-JUN-1999 99US-0139750
PR 22-JUN-1999 99US-0139613
PR 23-JUN-1999 99US-0139613
PR 23-JUN-1999 99US-0139613
PR 23-JUN-1999 99US-0140823
PR 23-JUN-1999 99US-0140823
PR 23-JUN-1999 99US-0140823
PR 23-JUN-1999 99US-0140823
PR 23-JUN-1999 99US-0142363
PR 23-JUN-1999 99US-0142363
PR 23-JUN-1999 99US-0142363
PR 23-JUN-1999 99US-0143362
PR 23-JUN-1999 99US-0143362
PR 23-JUN-1999 99US-0143362
PR 23-JUN-1999 99US-014332
PR 23-JUN-1999 99US-014332
PR 23-JUN-1999 99US-0144332
PR 23-JUN-1999 99US-0144333
PR 23-JUN-1999 99US-0144332
PR 23-JUN-1999 99US-0144332
PR 23-JUN-1999 99US-0144332
PR 23-JUN-1999 99US-0144332
PR 23-JUN-1999 99US-0144333
PR 22-JUN-1999 99US-0144333
PR 2
```

-

999

80

```
-----TACGGGTTCAAAGAGAGAAGAGA 927
                                                                                                            101 LeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrVal 120
                                                                                                                                                                                                                                                        161 GluLeuGlnGlnSerArgLysMetPheAlaSerMetTyrAlaLeuLys---ThrGluGly 179
                                                                                                                                                                                                        141 IleProAlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer
                                                                                                                                                                                                                                832 CTTCCAGGA---AGCAAATTCCTTTACGCCGATGTCTATAAT-----CCTATGATGGAG
               61 ThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGly
                                     607 TACCAAGACTTTATTCTTAAGAGGCTTGAAATTTTCGTGCGGGAGCTTTACAGTTTAGGT
                                                                                                                                   715 ATC---CATATGACTGCTAAATTCGCAACATTTTTAGATTCTGCTTGGAACACCATAAC
                                                                                                                                                           121 AspPheCysIleAlaTyrLysHisLysLeuProGlnLeuAsnAlaAlaGluLeuGly
                                                                                                                                                                                 772 AAAGACTCTGTTTTATACAATGAGAACTTCAGAATCTCTTGCCCCAAATCGAAGCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hybridisation assay, genetic mapping, gene expression control, protein identification, signal transduction pathway, metabolic pathway, promoter, termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana DNA fragment SEQ ID NO: 23034
                                                                                                                                                                                                                                                                                                                                                                             ЭЬ
                                                                                                                                                                                                                                                                             883 ATGATCCAAAACCCTAGCAAA-
                                                                                                                                                                                                                                                                                                                                                                             AAC39012 standard; DNA; 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0121825.
99US-0123548
99US-0125788.
99US-0125788.
99US-0125785.
99US-0127465.
99US-0127465.
99US-0128134.
99US-0128114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0130077
99US-0130449.
99US-0130891.
99US-0131449.
99US-0131449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0132407
99US-0132484.
99US-0132485.
99US-0132486.
99US-0132487.
                                                                                                                                                                                                                                                                                                     180 GlyValValAsrThr 184
                                                                                                                                                                                                                                                                                                                             928 GGATGTTGTGGAACA 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabicopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-1999
25-MAR-1999
25-MAR-1999
21-APR-1999
66-APR-1999
16-APR-1999
12-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                            17-CCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-200p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                    AAC39012;
                                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                  AAC39C
                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                          Ω.
                                                                                                                               Ω
                                                                                                                                                                                g
                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                           g
                                                                                                           ò
                                                                                                                                                           à
                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                     ò
                                                           \dot{S}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     547 ITCATTTGAACTATTACGAAATTCCCTCAAGGCGTCTCGAGTATCCTTTCATTCTGGT 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            487 AAGAAAGCGATGGAGATCATAAACAATGCCTTCGTGGTTGTGAGTGCAGGGCCTAACGAT 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 LysiysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGlu 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 SerAsnLeuSerAsnLeuVallleThrAspAlaSerSerLeuAsnGlyVal----Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 GlyIle-----GluValValPheGlyLeuLeuTyrAlaLeuAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11197
23
23
20
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-613-486-15 (1-198) x AAC45964 (1-1197)
9905-0151066
9905-0151066
9905-0151030
9905-0151303
9905-0151303
9905-0151303
9905-0151313
9905-0151313
9905-0151315
9905-0151315
9905-0154039
9905-0154039
9905-0154039
9905-0155486
9905-0155486
9905-0155486
9905-0155486
9905-0155486
9905-0155486
9905-0155486
9905-0155486
9905-0155486
9905-0155486
9905-0155486
9905-015933
9905-015933
9905-015933
9905-015933
9905-016081
9905-016081
9905-016081
9905-016081
9905-016081
9905-016081
9905-016081
9905-016081
9905-016081
9905-016081
9905-016081
9905-016081
9905-016081
9905-016081
9905-016081
9905-016130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.78
86.00
38.92%
26.49%
8.68%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                   21-007-1999
21-007-1999
21-007-1999
21-007-1999
22-007-1999
22-007-1999
22-007-1999
25-007-1999
25-007-1999
26-007-1999
                                                                                                                                20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
28-SEP-1999;
                                                                                                                                                                                                                                                                                       13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
                                                                                                                                                                                                                                                                 2-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                           15-SEP-1999
16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
```

à d

8 ें

ें g us-09-613-486-15.rng

Page 8

B
0
0
2003
Н
N
••
0
20
0
Ä
0
Н
>
Ò
Nov
-
ď
g
≅

99US-0145218. 99US-0145224.	00S-01	.10-SD6	0-S06	9US-014	0.03-01	9US-C1	9US-01	9US-01	0. Sn6	9US-014	- 10-SH6	9US-01	9.TS-014	9US-01	9US-014	9US-01	10-SD6	502-014	10-506	0.03-01	9US-014	9US-01	935-01	10-SO6	10-506	93S-019	9US-01	9US-01	9US-01	9US-01	9US-01	9US-01E	9US-018	0.CS-01	9US-01	9US-019	9US-015	9US-01	9US-01	10-SD6	erc-sne	9US-016	113-C18	0.00 - 0.	9US-01	TC-SAG	10-SU6	9US-015	9US-015	9US-015	210-506 2115-016	OUS-016	9US-016	913-016	3US-016	3US-016
666	6-JUL-1999	7 - JUL - 1999	7-JUL-1999	8-JUE-1999 7-217:1999	2-AUG-199	2-AUG-1999	4-AUG-1999	4-AUG-1999	5-AJG-1999	5 - AUG - 1999 5 - AUG - 1999	6-AUG-1999	9-AUG-1999	9-AUG-1999	0-AUG-1999	2-AUG-1999	3-AUG-1999	3-AUG-1999	5-AUG-1999	7 - AUG - 1999 8 - PI - 2 - 1999	0-AUG-1999	0-AUG-1999	0-AUG-1999	3-AUG-1999	3-AUG-1999	5-AUG-1999	7-AUG-1999	7-AUG-1999	7-AUG-1999	J-AUG-1999	1-SEP-1999	7-SEP-1999	0-SEP-1999	3-SEP-199 5-SED-199	5-SEP-199	0-SEP-199	2-SEP-199 3-SPD-199	4-SEP-199	3-SEP-199	9-SEF-199	6-00T-199	6-0CT-199	7-0CT-199	9-0C1-188	8-OCT-199	8-CCT-199	3-CCT-199	661-100-1 1-001-168	-0CT-199	1-0CT-199	1-0CT-199	661-100-1 	-0CT-199	1-0CT-199	-00T-199	0CT-199 0CT-199	3-0CT-199
9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	ማ የ	7. Y.	PR	יי ס א' ס	E E	G (r 0.	PR	다. IX	ጥ ወ ጽ ወ	PR N	P R	ማ ! የሩ !	or 0 0. 0	i ii	ያ የ	PR	ሟ ዊ ር	γ'	. Y.	PR	9.5R	ር! ር! (יינ איני	7. U.	. K.	PR	ሟ . ሚ .	አ ማ	7. A.G.	PR	PR t	አ ማ	PR	PR	y S	PR	7. C	7. 0 X 0	. K	PR	ር ር ር ር	יי נד היי נג	. E	ዋዋ	ц. Ц.	7 D	. D.	ጸ	ሟ ሺ ፤	7 G	PR	PR	טינ פילים	ኛ ሮ	PR
																	_	_											•					n																			-			_
ن ن	. :				٠.		: .:					<u>.</u>						•						: .:			٠.							.:		: :			• _:		•						. ,	.:								•
9US-0134256	9US-013 9US-013	OUS-013	9US-013	9US-013	9US-013	510-506 5115-013	9US-013	9US-013	SUS-013	9US-013	9US-013	9US-013	510-516	9US-013	9US-013	9US-013	9US-013	911S-0-3	9US-013	9US-013	9US-013	9US-013	112-013	9JS-013	9US-013	9US-013	9US-013	908-013 918-013	9US-014	9US-014	9US-014	9US-C14	9US-014	9JS-014	3US-014	9US-014	9US-014	40-506 418-014	9US-014	9US-014	3US-014	3US-014	9US-014	9US-014	9US-014	502-014 575-014	OUS-014	9.7S-014	9US-014	911S - 0 - 4	OUS-014	9US-014	3US-014	3US-014	3US-014	3US-014
6 6661		6 (6661	6 .666	6 (666)	6 16661	. 666	686	6561		6 1666	6 :666:	6 1666		6 666	6 1666	6 :666	999;		6 :666	6 :666	6 1666	6 . 600			6 1656	6 (666)	6 .666	, , , ,	6 666	6 1666	6 666		6 666	6 1666	999;	6 , 666	6 1666		6 666	6 (666	6 1666	999;	6 (666	6 1666	6 1666	A	6 666	6 1666	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	, no	6 666	6 666	6 .666	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6 666	e :666
11-MAY-1 14-MAY-1	14-MAY	14-MAY	18-MAY	20-MAY	21-MAY	25 - MAY	27-MAY.	28-MAY	200-10 201-10 20	04-40N	07-CUN-	.NU.2-80	NO - 01	14-CUN.	16-JUN-	16-JUN.	17-CON.	18-JUN-	18-JUN-	18-JUN-	18-JUN	LB-CCN-	NOD-61	18-JUN-	18-JUN-	18-JUN	18-JUN-	22 - TIN-	23 - JUN -	23 - JUN-	24 - JUN-	- NIII - 62	30-5UN-	01-JUL-	-JUL-10	- TOT- 90	08-JUL-	12-111	13-JUL-	14-JUL-	15-7JL-	16-JUL-	19-JUL-	19-JUL-	19-JUL-	100-8T	19-JUL-	20-JUL-	20-JUL-	21-JUL-	21-JUL-	21-JUL-	22-JUL 22-TTL-	22-JUL-	22-JUL-	23-JUL-
4 4 4 6 6 7	۲ K	2 6	n n n	PR	20,00	4 64	PR	25	7, 0 7, 0	25	22	8 5	ν α κ α	. E	8	2	α p	4 pg	E E	ظ	<u>بر</u>	χ. p	4 0	α.	8	8.	מי נ	K PK	2	۲.	2 6	¥ 04	ŭ,	8	X 0	£ 64	ŭ,	۲ A	. a.	PR	8 5	4 24	PR	53	<u>د</u> د	χ. α	<u> </u>	8.5	¥ 0	4 24	8	8 5	χ. p.	ď	Œ I	œ

```
489 AAGAAAGCGATGGAGATCATAAACAATGCCTTCGTGGTTGTGAGTGCAGGGCCTAACGAT 548
                                                                                                                                                                                                                                                                                                                                                                                                                               609 TACCAAGACTTTATTCTTAAGAGGCTTGAAAATTTCGTGCGGGAGCTTTACAGTTTAGGT 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 LeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrVai 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AspPheCysIleAlaTyrLysHisLysheuProGlnLeuAsnAlaAlaAlaGluLeuGly 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    774 AAAGACTCTGTTTTATACAATGAGAACTTCAGAATCTCTTGCCCCAAATGGAAGCATCT 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lleProAlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :::||||
834 CTICCAGGA---AGCAAATICCTTTACGCCGATGTCTATAAT-----CCCATGATGAG 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlubeugingInSerArgLysMetPheAlaSerMetTyrAlaLeuLys---ThrGluGly 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---racegettcaagagacgaagaga 929
                                                                                                                                                                                                                                                                                                                                 429 TCGGAACAACCAAACATGTTCAAGAGTTACATTGCTCGTCTCAAAGGTATCGTGGGAGAC 488
                                                                                                                                                                                                                                                                                                        SerAsnLeuSerAsnLeuVallleThrAspAlaSerSerLeuAsnGlyVal-----Asp 24
                                                                                                                                                                                                                                                                                                                                                        LysLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGlu 44
                                                                                                                                                                                                                                                                                                                                                                                                              ----GluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGly 80
                                                                                                                                                                                      1199
49
23
93
20
                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                               US-09-613-486-15 (1-198) x AAC39012 (1-1199)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrococcus abyssi genomic fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF86431 standard; DNA; 349980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGATCCAAAACCCTAGCAAA
           99US-0160989.
99US-0161404.
99US-0161405.
99US-0161405.
99US-016136.
99US-016136.
99US-0161920.
99US-0161992.
99US-0161993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyValValAsnThr 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              930 GCATGTTGTGGAACA 944
                                                                                                                                                                                   0.782
86.00
38.92%
26.49%
8.68%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                              Glylle
           22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-2001
                                                                                                                                                                         Alignment Scores:
                                                                                                                   28-OCT-1999
                                                                                                        28-OCT-1999
                                                                                                                                             29-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  717
                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                          25
                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF86431;
                                                                                                                                                                                      Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF86431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ω̈́ρ
Cp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΩΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

```
138176 GCAAGGCTACCATCTACCCCCGAGACAATATACGGAATTGGTTCAATAACCAAGAGCTTT 138235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138056 AAATTGGAGGCTTCATAGTTGAAAAATGGCTGAAAGGAAA---GTTCCTGGGATAAGC 138112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AAAGATGGGGACGTTGTCTATGCAAAGGGCTTTGGATACAGAAATGTTGAG 138175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the genomic sequence of Pyrococcus abyss; and P. abyss; proteins (see AAB96637.AAB96842). P. abyssi is a hypothermobhilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. abyss. The 3 rend of this sequence overlaps with the 5 end of AAH41223. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to Note: This patent is in the same patent family as WO200065052, which contains additional sequences as shown in AAB99132-AAB99143,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --ValvalThrGluGlyAspLeuLysLysValLeuAspGly 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 ValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGlyGluArgAsnVal---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleGluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLys
                                                                                                              ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 349980 BP; 95167 A; 78444 C; 78870 G; 97499 T; C other;
                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleotide sequences isolated from Pyrococcus abyssi encode
proteins useful in industry -
                                                             Location/Qualifiers
300001.349980
/hote= "This sequence overlaps with the 5' end
/note= "This sequence overlaps with the 5' end
                                                                                                                                                                                                                                                                                                                                          Lecompte D;
 ds.
Hyperthermophilic archaeon; hyperthermophilic protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thierry JC, Prieur D, Dietrich J,
Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-613-486-15 (1-198) x AAF86431 (1-349980)
                                                                                                                                                                                                                                                                                          (CNRS ) CNRS CENT NAT RECH SCI.
(IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 183-279; 1657pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.99e+03
86.00
35.71%
25.97%
8.68%
                                                                                                                                                                                                                               99FR-0005C34
                                                                                                                                                                                                                                                            99FR-0005C34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138113 ATTAGCATAATT----
                                                                                                                              AAH41223"
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-126236/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                              Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                        Forterre P, 1
Querellou J,
                                                                                                                                                                                                                             21-APR-1999;
                                                                                misc_feature
                                                                                                                                                                                                                                                            21-APR-1999;
                                                                                                                                                              FR2792651-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                             27-0CT-20C0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
No
 ΩΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΩΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

ò

g

DD.

ò

qq

ò

qq

```
2395 GITITCGAAAAATATTAGAITTATCATTAAAAGATTCAAGATTAACTAATAAGITTTTG 2454
                                                                                                                                                                                                                                                                                                                                                                                                      2179 ITTITIGAAAATAITACITCAACTAATICCAACGACAAGIGGATTAAAGAAATAAGCAAT 2238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2398 GATACTAAAAATATA---GACAATATCTTTTCGAAAAGAAACATGGTTACCAATTTAAT 2394
                                                                                                                                                                                                                                                 30 AspleulystysValleuAspGlyCysAlaProLeuThrArgPheThrAsnLysLeuArg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLRav-5, grapevine leafroll virus, GLRav infection, GLRav coat protein, GLRav HSP70 homologue protein; viral gene mapping, plant disease resistance, ds.
                                                                                                                                                                                                               ---SerAsnLeuValileThrAsp---
                                                                                                                                                                                                                                                                                                                              2119 AAAACGAAAGTIGACAATITCCCGITIGITGAIAAATCGAGIAAATCGGATATITITICI
                                                                                                                                                                                                                                                                                                                                                                    ------hlaSerSerLeuAsnGlyValAspLys-----LysLeuSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                              31 GluValGluLysMetLeuValGlrLysGlyAlaProAsnGluGly---IleGluValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.9 TTTATAGATTATTGTGTGAATGAAGAACATTTAGGGAATAAGGGAGCTATAAAATGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProlysValGlnArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 AspSerAspValIlePheSerAsnSerPheGlyGluArgAsnValValThrGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "No start codon given; Specifically claimed
                                      "HSP70 homologous protein"
                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product= "ORF 2 protein"
hote= "Specifically claimed
285..4094
                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product= "coat protein"
                                                                                                                                                                         US-09-613-486-15 (1-198) x AAT68648 (1-4467)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTITICITIGAAATAITAATGAA 2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 ThrPheGlyArgThrPheThrGlu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                               2 GluLeuMetSerAspSerAsnLeu--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA91259 standard; DNA; 4766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLRaV-5 nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574..2989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag= a
product=
                                        7.09
85.00
41.89%
24.32%
8.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grapevine leafroll virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .1593
                                                                                                                                                                                                                                                                                           16 -----
                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-XAY-2001
                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA91259;
                                      No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA91255
                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            엄
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                   DD.
                                                                                                                                                                                                                                                                                                                       CC
                                                                                                                                                                                                                                                                                                                                                                \delta
                                                                                                                                                                                                                                                                                                                                                                                                  CD
                                                                                                                                                                                                                                                                                                                                                                                                                                      \dot{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \dot{\circ}
138236 ACAGCCTTGGCAATAATGAAATTAGTGGAAGAGGGCGGATTAAGT-----TTGGATGAC 138289
                                                                            138290 -----CCCGTTGAGAAATTCGTTAATATAAAGCTTAGACCATTCGGAGAACCAGTGACC 138343
                                                                                                                                                    138344 -----GTTCATCACCTGTTAACGCATTCCTCGGGGATTCCATCTTAGGATATGCC 138394
                                                                                                                  136
                                        CysalaProLeuThrArgPheThrAsn -- LysLeuArgThrPheGlyArgThrPheThr
                                                                                                                  117 GlualaryrvalaspPheCysllealaryrLysHisLysLeuProGlnLeuAsnAlaala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The 4.5 kb EcoRI fragment (AAT68648) of plasmid pSRQ800 includes a coding sequence for AbiE (AAW1788), a protein which, in Lactococcus lactis (L.l.), increases resistance to phages by aborting infection. pSRQ800 was isolated through examination of the phage resistance mechanism of L.l. subsp. lactis W1. The total plasmid DNA of W1 was co-electroporated with shuttle vector pSA3 into phage-sensitive, plasmid-free L. lactis LM0230. Phage-resistant transformants were isolated and found to contain pSRQ800. The isolated DNA can be used to impart phage resistance to bacteria, esp. L.l., for use in the prodn. of fermented dairy
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AbiE, phage abortive infection protein, phage resistance, pSRQ800, lactic acid bacterium, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated DNA encoding the AbiE protein of Lactococcus - for protecting strains used in production of fermented dairy products
                                                                                                                                                                                                                   138395 GAGGCCTTCATAGACGGAATGGTCGGTGGGGATAACTGGTTG 138436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4467 BP; 1583 A; 668 C; 643 G; 1573 T; 0 other;
                                                                                                                                                                                           137 AlaGluleu----GlylleProAlaGluAspSerTyrLeu 148
                                                                                                                                                                                                                                                                                                                                                                                                                          pSRQ800 fragment including coding sequence for AblE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vandenbergh PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactococcus lactis subsp. lactis isolate Wl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moineau S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 29-32; 49pp; English
                                                                                                                                                                                                                                                                                                           AAT68648 standard; DNA; 4467 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-IB01385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0565907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1203..1207

/*tag= a

1225..1230

/*tag= b

1265..1271

/*tag= c

1279..3078
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holler BJ, Kondo JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNIL ) QUEST INT BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-319765/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW17788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vedamuthu ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9720917-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :9661-ACN-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
-35_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -10_signal
```

RBS CDS products

49

us-09-613-486-15.rng

Page 11

FT FT

XXXXXXX

```
The present invention describes a gene (1) derived from Buchnera sp. containing the DNA (a) or (b), (a) has a fully defined base pair sequence selected from a table of sequences found in the Buchnera sp. genemic DNA of ABA92787 given in the specification or is a DNA selected from complementary DNA sequences, and (b) is a DNA which hybridises with the DNA (a) and encodes a protein. Also described are: (1) a recombinant vector (11) containing (1); (2) a transformant (111) containing (11); (3) a genomic DNA of Buchnera sp. containing the sequence given in ABA92787; (4) a plasmid derived from Buchnera sp. containing DNA (c) or (d), (c) is a DNA containing a fully defined sequence given in ABA92786 or ABB92789 and (d) is a plasmid which hybridises with a DNA; and (5) a method for the preparation of a protein in which (III) is cultured and the expression protein of the objective protein is collected from the cresultant culture. The DNA is useful for developing agricultural chemicals for exterminating cockroaches. The present sequence represents the specifically claimed Buchnera sp. genomic DNA sequence from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435915 AAAAATCAACGTGGATCATTAAGCATTGATGACGAAGGTACTCCAGGTCAAAGAATAT. 435856
                               -----AspSerTyrLeuAlaAlaASpPheLeuGlyThrCysProLysLeuSerGluleu 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGlyGluArgAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 640681 BP; 237522 A; 83822 C; 84757 G; 234580 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                   Buchnera; cockroach-symbiotic bacterium; cockroach extermination;
circular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32
26
53
53
53
                                                                                                                         4014 TCCAATAGCAACAGGCTACACACAATCTGTAC 4046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic DNA of cockroach-symbiotic bacterium
                                                                                            163 GlnGlnSerArgLysMetPheAlaSerMetTyr 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-613-486-15 (1-198) x ABA92787 (1-640681)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 16-230; 237pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                         Buchnera sp. genomic DNA SEQ ID NC:1.
                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                 ABA92787 standard; DNA; 640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-APR-2000; 2000JP-0107160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37-AFR-2000; 2000JP-0107160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RIKA ) RIKAGAKU KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.5e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.50
37.18%
20.51%
8.43%
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-126043/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP2001292771-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                           27-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchnera sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                               ABA92787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                         ABA92787/c
                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3720 GGTAAGGAAGTGACACTTGCCCCATGATGAGATAAAGACAGCTCTAGACAATTCTATAGGG 3779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3897 GTGCCGCCTAACTACTATCCTTACTCGCCAGACTGTCTGCATGTTGATGCAAGACTGTTC 3956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a grapevine leafroll virus (GLRaV-5) DNA sequence of the invention. The DNA sequence can be used in an expression construct. The construct is useful for providing resistance to GLRaV infection in a recombinant plant cell by transforming the plant cell with it, where transcription of the polynucleotide sequence interferes with normal viral function such as movement, encapsidation or replication of viral RNA. The polynucleotide sequence is expressed as an antisense sequence and encodes a GLRaV coat protein, preferably a defective GLRaV coat protein or a GLRaV HSP70 homologue protein. The GLRaV-5 DNA is useful for the synthesis of GLRaV, as diagnostics and probes, for viral gene mapping and for induced plant disease resistance. It Is also useful to detect and quantitate expression of GLRaV in plant tissue prior to use in vegetative propagation, by detecting the presence of GLRAV RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluArgAsnValValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10. LeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AspPheCysIleAlaTyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGly 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel grapevine leafroll virus polynucleotide useful as diagnostic and probe, for viral gene mapping and for induced plant disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3780 TCTTTCGGTTACGAAAACACTCCTAGACAATTTGGAAGAGCATTCACGGCAGCGATAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3840 CAAGGGATATCCTCAGGCAAACTGGAGGTG----AACACGAAGATCTGCGGTTTCTCACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4766 BP; 1329 A; 890 C; 1231 G; 1316 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4766
32
21
21
57
21
                                                                 /product= "duplicate coat protein"
/note= "Specifically claimed region"
"Specifically claimed region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB: AAY97688, AAY97689, AAY97690, AAY97691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-613-486-15 (1-198) x AAA91259 (1-4766)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 IleProAlaGlu-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 60pp; English.
                                                                                                                                                                                                                                 2000WO-US19708:
                                                                                                                                                                                                                                                                             99US-0144453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.03
84.03
40.468
2.54.468
22.8488
                     4128..4751
/*tag= d
    ncte=
                                                                                                                                                                                                                                                                                                                           (AGRI-) AGRITOPE INC
                                                                                                                                                                                                                                                                                                                                                                                                                   2001-147339/15
                                                                                                                                                                                                                                                                                                                                                                         Good XC, Monis J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                          W0200105957-A2
                                                                                                                                                                                                                                 19-JUL-2000;
                                                                                                                                                                                                                                                                             19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                   25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
```

g

ò

g

ò

d $\dot{\delta}$ g ठ

ò

ઠે

8 c c ò

```
526 GCAGAAGTAAATTATTTACCTGAAGCGCATGAGGATTTCTTAGTTTCAGATTCAAGCGAG 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaAlaGluLeuGlyIleProAlaGluAsp 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         586 TATAATGACAAACTAAATATCAACTTTGCTTTGGGTCTAGGGGTCAGCGAGTTTATT 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 SerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 AGATTAACGATTCCTGAACTTGATGAAGCÄTACGTTGATTTACTCGTGAATTACGAGGTG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466 CCCTTAGAAGCATTTATAGTTCCTCTAAGAGTTAGAATTCGTAGTATGAATTGCT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------AACCGGCTCGAAAATATGATGGAAAAA 678
This sequence represents DNA encoding a 46.5 kD immunogenic fragment of the protective polypeptide antigen (PPA) of the bacterium Erysipelothrix rhusiopathiae. This bacterium infects livestock, particularly pigs (swine erysipelas), and is also able to cause disease in humans. The recombinantly produced PPA fragment may be used as a subunit vaccine for simulating an immune response in animals against Erysipelothrix rhusiopathiae. As the vaccine can be produced recombinantly, it can be produced on a large scale. The vaccine is suitable for transmucous
                                                                                                                                                                                                                                                                                                                                                                                                                                    60 ArgThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSerAsnSerPhe 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Erysipelothrix rhusiopathiae full-length PPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protective polypeptide antigen; PPA; Fujisawa strain; swine erysipelas; recombinant production; immunogenic; subunit vaccine; transmucous administration; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G.yGluArgAsnValValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACACCGTATTTTAGTAAAATATGAAGGTAAAGTTTAAA------GGTAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GluAlaTyrValAspPheCysIleAla------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProleuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThr----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88..1293
/*tag= b
/product= "Erysipelothrix rhusiopatriae 46.5 kD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erysipelothrix rhusiopathiae full-length PPA coding sequence
                                                                                                                                                                                                 Seguence 1209 BP; 456 A; 177 C; 237 G; 339 T; 0 other
                                                                                                                                                                                                                                                          1209
333
21
50
29
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ArgiysMetPheAlaSerMetTyrAlaLeuLys 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           679 GAACTICATCCACTGTATCTIGAACTTTATGCTATGCGG 717
                                                                                                                                                                                                                                                                                               Conservative:
                                                                                                                                                                                                                                                                                                                      Mismatches:
                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                               US-09-613-486-15 (1-198) x AAA72313 (1-1209)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA72318 standard; DNA; 1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erysipelothrix rhusiopathiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / cag= a
/product= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                        2.97
81.50
40.60%
24.81%
8.22%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...1881
*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         646 GACTAT-----
                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                administration
                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-2000
                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126
                                                                                                                                                                                                                                                                                                                                Query Match:
DB:
                                                                                                                                                                                                                                                            No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dC
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                        ---ACCTATATG 435718
                                                                                                                                                                                                                                                                                                                                                        ----TATGCTGTAAATTTTTCTGGA------GGACAGGTAGATATTACT 435625
                                                                                                                                                                                                                                                                                                                                                                                                                        435624 TCCGGAAAATTTCTATTTCTACTTCGGAAGCTTATTAATAAAAAGGAAAAATTGTT 435565
                                       435855 TTAATTGAAAATGGAATATTAAAAAAAATATATGCAAGATAAACTTAATGCGGGTTTAATG 435796
                                                                                                                                                            PheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCys 123
                                                                                                                                                                                                                                                                                                               144 GlukspSerTyrieuAlaklakspPheLeuGlyThrCysProLysLeuSerGluLeuGln 163
                                                                                                                                                                                                                                                                                                                                                                                             164 GlnSerArgLysMetPheAlaSerWetTyrAlaLeuLysThrGluGlyGlyValValAsn 183
                                                                                  --GlyCysAlaProLeuThrArg 103
    96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "No initiation or termination coden given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        swine erysipelas;
                                                                                                                                                                                                                                     124 lleAlaTyrLysHisLysLeuProGlnLeuAsrAlaAlaAlaGluLeuGlyIleProAla
                                                                                                                                                                                                                                                              il recombinant protective polypeptide antigen useful as a vaccine protecting livestock against Erysipelothrix rhusiopathiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a /*tag= // product= "Erysipelothxix rhusiopathiae 46.5 kD PPA / product= fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435564 ACACCAATTAAAACACTACTCTCATAGGATCAGGATTAGAAGTTATG 435517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrFroValSerAsnieuArgGinLeuGlyArg---ArgGluValMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protective polypeptide antigen; PPA; Fujisawa strain; recombinant production; immunogenic; subunit vaccine; transmucous administration; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NORQ ) NORINSUSANSHO KACHIKU EISEI SHIKENJOCHO (HGET ) HIGETA SHOYU KK. (FUJI-): FUCITA GAKUEN.
  ValValThrGluGlyAspieurysLysValLeuAsp--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erysipelothrix rhusiopathiae PFA fragment DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Fig 4A-4C; 23pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA72313 standard; DNA; 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erysipelothrix rhusiopathiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-00943C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-00943C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                              435735 ATGACTAAT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-551432/51.
P-PSDB; AAB14800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP3072345-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for protecinfection
                                                                                                                                                            104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA72313;
                                                                                                                                                                                                                                                                                                                                                        435663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA72313
                                                                                                                                                                                              g
                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                S
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cp
                                       g
```

```
Alignment Scores:
                                                                                                                                                                                                                                                                                                                 RBS
                                                                                                                                                                                                                                                                                                                                               Soc
                                AAA50205
                                                            613 GCAGAAGTAAATTATTTACCTGAAGCGCATGAGGATTTCTTAGTTTCAGATTCAAGCGAG 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAsp 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          673 TATAATGACAAACTAAATAATATCAACTTTGCTTTGGGTCTAGGGGTCAGCGAGTTTATT 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer 165
                                                                                                                                                                                                                                                                                                                                       The invention relates to a 46.5 kD immunogenic fragment (AAB14800) of the protective polypeptide antigen (PPA) of the bacterium Erysipelothrix Thusiopathiae, and to DNA encoding it (AAA72113). This bacterium infects livestock, particularly pigs (swine erysipelas), and is also able to cause disease in humans. The recombinantly produced PPA fragment may be used as a subunit vaccine for stimulating an immune response in animals against Erysipelothrix rhusiopathiae. As the vaccine can be produced recombinantly, it can be produced on a large scale. The vaccine is suitable for transmucous administration. The present sequence represents the coding sequence of DNA encoding the full-length PPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 GlyGluArgAs:NalValValThrGluGiyAspLeuLysLysValLeuAspGlyCysAla 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgThrThrSerProLysValGinArgAlaAspSerAspValllePreSerAsnSerPhe 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 AGATTAACGATTCCTGAACTTGAAGAAACATACGTTGATTACTCGTGAATTACGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            505 AAACACCGTATTTTAGTAAAATATGAAGGTAAAGTTAAA-------GGTAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProbeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GluAlaTyrValAspPheCysLeAla------
                                                                                                                                                                                                                                                      il recombinant protective polypeptide antigen useful as a vaccine protecting livestock against Erysipelothrix rhusiopathiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1881 BP; 719 A; 291 C; 384 G; 487 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1881
33
21
20
50
50
50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 -----ArgLysMetPheAlaSerMetTyrAlaLeuLys 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        766 GAACTICATCCACTGTATCTTGAACTTTATGCTATGCG 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                             NORQ) NORINSUSANSHO KACHIKU EISEI SHIKENJOCHO.
HGET) HIGETA SHOYU KK.
(FUJI-) FUJITA QAKUEN.
fragment (AAB14800)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-613-486-15 (1-198) x AAA72318 (1-1881)
                                                                                                                                                                                                                                                                                                              Example 1; Fig 2; 23pp; Japanese.
                                                                                      99JP-0094004
                                                                                                                  99JP-0094004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.65
81.50
40.60%
24.81%
8.22%
                                                                                                                                                                                                        WPI; 2000-551432/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                         P-PSDB; AAB14800
                           JP3072345-B1
                                                                                                                  31-MAR-1999;
                                                                                      31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                         31-JUL-2000
                                                                                                                                                                                                                                                                                    infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
Score:
                                                                                                                                                                                                                                                      Novel
```

g ò d

ਨੇ

d à Ω Ω

ò

g

ò

d

ò

ò

```
The present sequence is that of the Bpa gene of strain Fujisawa of Erysipelothrix rhusiopathiae, the causative agent of erysipelas in animals and erysipeloid in humans. The gene encodes a protective antigen (see AAY95782), termed erysipelas protective antigen (spa AAY95782), termed erysipelas protective antigen (spa AAY95782). The was isolated from a genomic DNA library of strain pujisawa by immunoscreening using E. rhusiopathiae convalescent pag serum. The N-terminal portion of the Bpa protein, was isolated comprising residues 12-195 of the protein, was identified as a vaccine antigen. The N-terminal polypeptide was identified as a vaccine antigen. The N-terminal polypeptide comprises of E. rhusiopathiae, where the immunogenic polypeptides of E. rhusiopathiae, where the immunogenic polypeptides comprises an immuno-protective epitope from the N-terminal region of Epa, especially a turkey or pig, from infecting an animal, especially a turkey or pig, from infection by E. rhusiopathiae involves administering the vaccine, or an expression vector comprising a nucleic acid encoding the N-terminal region or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccines for protecting turkeys and pigs against Erysipelothrix rhusiopathiae infections comprising a polypeptide sequence from the N-terminal region of an erysipelas protective antigen -
                                                                                                                                                                                                                                                Erysipelas protective antigen; Epa; SpaA.1; DNA vaccine; infection;
                                                                                                                                                                                     Erysipelothrix rhusiopathiae erysipelas protective antigen gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2040 BP; 776 A; 293 C; 418 G; 553 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
AAA50205 standard; DNA; 2040 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example, Fig 2; 61pp; English.
                                                                                                                                                                                                                                                                                                                                          Srysipelothrix rhusiopathiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-FEB-2000; 2000WO-US03789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0119389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= c
100..1980
/*tag= d
100..186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= e
187..1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimoji Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYRC ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-length Epa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
65..70
/*tag=
88..92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                        41..46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-524541/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAY95782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200047744-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fischetti VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-FEB-1999;
                                                                                                                        07-NCV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-AJG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sig_peptide
                                                                                                                                                                                                                                                   Erysipelas
                                                                                                                                                                                                                                                                                                                                                                                                                                        -35_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -10_signal
                                                             AAA50205;
```

```
2000-551432/51
                       F-PSDB; AAB14800
                                                                                                                                                                                                                                                          Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166
                                                                                                                                                                                                                                                                                                                Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search con
Job time
                                                                                                                                                                                                                                                                                Score:
   9
                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          े
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                      712 GCAGAAGTAAATTATTACCTGAAGGCATGAAGGATTTCTTAGTTTCAGATTCAAGCGAG 771
                                                                                                                                                            126 TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAsp 145
                                                                                                                                                                                                                                                                                                                            146 SerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer 165
                                                                                                                                                                                                                                                                                                                                                 ------AACCGGCTCGAAAATATGATGGAAAAA 864
                                                                                                                       544 AGATTAACGATTCCTGAACTTGATGAAGCÄTACGTTGÄTTTACTCGTGAATTACGAGGTG 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "Erysipelothrix rhusiopathiae full-length PPA"
487..1692
                                                                                                  60 ArgThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSerAsnSerPhe 79
                                                                                                                                               80 GlyGluArgAsnValValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAla 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujisawa strain; swine erysipelas; subunit vaccine;
                                                                                                                                                                                                                                    772 TATAATGACAAACTAAATAATATCAACTTTGCTTTGGGTCTAGGGGTCAGCGAGTTTATT
                                                                                                                                                                                        ProcenthrargphethrasniysLeuargthrPheGlyargthrPhethr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Brysipelothrix rhusiopathiae 46.5 kD PPA
fragment (AAB14800)"
2040
33
21
50
29
                                                                                                                                                                                                                                                                                                                                                                       ----ArglysMetPheAlaSerMetTyrAlaLeuLys 176
                                                                                                                                                                                                                                                                                                                                                                                          865 GAACTICATCCACTGTATCTICAACTTTATGCTATGCGG 903
           Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erysipelothrix rhusiopathiae full-length PPA DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NORQ ) NORINSUSANSHO KACHIKU EISEI SHIKENJOCHO.
(HGET ) HIGETA SHOYU KK.
(FUJI-) FUJITA GAKUEN.
 Length:
                                                       Gaps:
                                                                             US-09-613-486-15 (1-198) x AAA50205 (1-2040)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protective polypeptide antigen; PPA; recombinant production; immunogenic; transmucous administration; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA72317 standard; DNA; 2814 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erysipelothrix rhusiopathiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0094004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0094004
6.36
81.50
40.60%
24.81%
8.22%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100..2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP3072345-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
                                                                                                                                                                                                                                    117
                                                                                                                                                                                        100
                                                                                                                                                                                                                                                                                                                                                                       166
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA72317
 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                             4AA72317
              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FXSXXXXXX
                                                                                                   ò
                                                                                                                      g
                                                                                                                                              ò
                                                                                                                                                                   a
                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                        ò
                                                                                                                                                                                                                                     ਨੇ
                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                            ે
```

```
1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [111] GCAGAAGTAAATTATTACCTGAAGCGCATGAGGATTTCTTAGTTTCAGATTCAAGCGAG 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AACCGGCTCGAAATATGATGGAAAAA 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 SerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSer 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      952
                                                                                                                                                                                                The invention relates to a 46.5 kD immunogenic fragment (AAB14860) of the protective polypeptide antigen (PPA) of the bacterium Erysipelothrix rhusiopethiae, and to DNA encoding it (AAA72313). This bacterium infects livestock, particularly pigs (whine erysipelas), and is also able to cause disease in humans. The recombinantly produced PPA fragment may be used as a subunit vaccine for stimulating an immune response in animals against Erysipelothrix rhusiopathiae. As the vaccine can be produced recombinantly, it can be produced on a large scale. The vaccine is suitable for transmucous administration. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 ArgThrThrSerProLysValGinArgAlaAspSerAspValllePheSerAsnSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .072 TATAATGACAAACTAAATAATATCAACTTTGCTTTGGGTCTAGGGGTCAGGGAGTTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 GlyGluArgAsnValValValThrGluGlyAspleuLysLysValLeuAspGlyCysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 ProLeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThr------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              952 CCCTTAGAAGCATTTATAGTTCCTCTAAGAGATAGAATTCGTAGTATGAATTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGiyIleProAlaGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 -------GluA aTyrValAspPheCysIleAla-----
Novel recombinant protective polypeptide antigen useful as a vaccine for protecting livestock against Erysipelothrix rhusiopathiae infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 2814 BP; 1048 A; 439 C; 558 G; 799 T; 0 cther;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAACTICATCCACTGTATCTTGAACTTTATGCTATGCGG 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ArgLysMetPheAlaSerMetTyrAlaLeuLys 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8, 2003, 01:41:31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-613-486-15 (1-198) x AAA72317 (1-2814)
                                                                                                                                    Example 1; Fig 1A-1B; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding the full-length PPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.1
81.50
40.60%
24.81%
8.22%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               completed: November
Ne : 383 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1132 GACTAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
```

Page

Sequence 3735, Ap Sequence 3735, Ap Sequence 384, Ap Sequence 15086, A Sequence 17, Appli Sequence 7, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 15, Appli Sequence 15, Appli Sequence 20, Appli Sequence 21, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 37, Appli

us-09-613-486-15.rni

```
GENERAL INFORMATION:

APPLICANT: Zhu, Hai-Ying
APPLICANT: Zhu, Hai-Ying
APPLICANT: Zhu, Hai-Ying
APPLICANT: Zhu, Hai-Ying
APPLICANT: Consalves, Dennis
TITLE OF INVENTION: AND THEIR USES
TITLE OF INVENTION: AND THEIR USES
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADRRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PROPER PLOPS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURSTRING SYSTEM: DC-DOS/MS-DOS
CURSTRING NUMBER: US/09/080,983
FILING DATE:
CLASSIFICATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 60/047,194
FILING DATE: 20-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,707
REFERENCE/DOCKET NUMBER: 19603/1631
TELECOMMUNICATION INFORMATION:
4 US-09-252-991A-3636

4 US-09-252-991A-3636

4 US-09-252-991A-1824

4 US-09-252-991A-16286

4 US-09-252-991A-16516

1 US-08-252-991A-16516

1 US-08-252-991A-16516

1 US-08-451-777A-7

2 US-08-451-777A-7

2 US-08-451-777A-7

5 PCT-US9-06748-7

5 PCT-US9-06748-7

5 US-09-080-983-12

4 US-09-1285-601-1

1 US-08-484-105-15

1 US-08-484-105-15

1 US-08-484-105-15

1 US-08-948-155-50

2 US-09-944-105-15

1 US-08-948-105-15

1 US-08-948-105-15

1 US-08-948-105-15

1 US-08-948-105-15

1 US-08-948-105-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 US-09-103-840A-2

3 US-09-103-840A-1

US-09-422-80-1

US-09-978-197-3

US-09-273-107-3

US-08-276-152-120

US-08-576-165-3

US-08-576-165-3

US-09-670-374-261

US-09-670-374-261

US-09-670-374-261

US-09-670-374-261

US-09-522-991A-15531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09380983 Patent No. 6197948
              1233 4 US

1491 4 US

1776 4 US

1776 4 US

1776 7 676 2 U

7676 2 U

7776 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-09-080-983-14
                Command line parameters:
-MODEL=frame + p2n.model -DEV=Xlh
-QE/G9D2_1/USPTO_spool/USO9613486/runat_C7112003_12041i_27115/app_query.fasta_1.391
-QE/G9D2_1/USPTO_spool/USO9613486/runat_C7112003_12041i_27115/app_query.fasta_1.391
-QE/G9D2_1/USPTO_spool/USO9613486/runat_C7112003_12041i_-MATRIX=DISSUGG_PE0
-LOOPEXTO_-UNITS=Dits -START=1 -END=-1 -MATRIX=DISSUGG_PENSSHDMMANG_0.Cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=ECt -THR_MAX=100 -THR_MINE_0 -ALIGN=15
-USR=USO9613486 @CGN 1 1 56 @runat_07112003_120411_27115 -NCPU=6 -TCPU=3
-NO_MMAP -LARGEQUERY -NGG_SCORES_C -MAIT -DSPBLOCK=100 -LONGLOG
-NO_MMAP -LARGEQUERY -NGG_SCORES_C -MAIT -DSPBLOCK=100 -LONGLOG
-NGG_SCORES_C -MARN_TIMEOUT=120 -WARN_TIMEOUT=120 -WARN_TIMEOUT=120 -WARN_TIMEOUT=120 -WARN_TIMEOUT=120 -WARN_TIMEOUT=100 -LONGLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Appl
Sequence 1, Appl:
Sequence 1, Appl:
Sequence 1, Appl:
Sequence 1, Appl:
Sequence 13503, A
Sequence 13503, A
Sequence 13503, A
Sequence 13503, A
Sequence 15, Appl:
Sequence 15, Appl:
Sequence 15, Appl:
                                                                                                                                                               7, 2003, 23:44:24; Search time 63 Seconds (without alignments) 1387.204 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                       1 MELMSDSNLSNLVITDASSL......GGVVNTPVSNLRQLGRREVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    issued_Patents_NA:*
i: /dgn2_6/ptodata/2/ina/5A_COMB.seq:*
cgn2_6/ptodata/2/ina/5B_COMB.seq:*
i: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
d: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/FUTCS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PatTCS_COMB.seq:*
                                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-080-983-14
US-09-280-983-1
US-08-522-991A-1531
US-08-565-907A-1
US-08-910-551B-1
US-08-9910-551B-1
US-09-252-991A-13503
US-09-252-991A-13503
US-09-252-991A-1350
US-09-252-991A-1350
US-09-253-991A-1350
US-09-253-15
                                                                                                                              nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     569978 seqs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                  Xgapop 10.0 , Xgapext (Ygapop 10.0 , Ygapext (Fgapop 6.0 , Fgapext Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                           US-09-613-486-15
991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    597
15500
2014
4467
4467
4467
1743
2139
2433
1434
536165
                                                                                                                                                                      November
                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99911885
865
885
885
885
885
887
881
881
897
967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB s
Maximum DB s
                                                                                                                            OM protein
                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jatabase
                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
```

Seguence 261, App Seguence 15531, A

Seguence

Sequence 3 Sequence 3 Sequence 4 Sequence 5 Sequence 5 Sequence 5

```
ThringserproLysValGinArgAlaAspSerAspValilePheSerAsnSerPheGiy 80 [[[[[[]]]]]][[[]]]]] ACCAGGTCTCCTAAGGTTCAGGGGGGAGATTCAGACGTTTATATTTCAAATAGTTTCGAA 240
                                                                                                                                                                                                                                                                                                                                                                                                           GluargasnValValValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuThrargPheThrasnLysLeuArgThrPheGlyargThrPheThrGlualaryrVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 IleProAlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                       21 AsrGlyValAsplysLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                            GlubeuGlnGinSerArgiysMerPheAlaSerMetTyrAlaLeulysThrGluGlyGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATTACAGCAAAGTAGGAAGATGTTCGCGAGTATGTACGTCCTAAAAACTGAAGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/C9080983
Patent No. 6197948
GENEALINFORMATION:
APPLICANT: Zhu, Hai-Ying
APPLICANT: Ling, Kai-Shu
APPLICANT: Consalves, Dermis
TITLE OF INVENTION: GRAPEVINE LEARROLL VIRUS TYPE 2 PROTEINS
TITLE OF INVENTION: AND THEIR USES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                             597
597
598
599
                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                       US-09-613-486-15 (1-198) x US-39-080-983-14 (1-597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nixon, Hargrave, Devans & Doyle
                                                                                                                                                                                    Gaps:
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                            01e-127
                                                                                                                                     991.00
100.00%
100.00%
                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-080-983-1
                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                     191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541
                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161
                                                                                                                            Pred. Nc.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
                                                                                                                                      Score:
                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                 Dp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                    35
                                                                                                                                                                                                                                                                                                                                                               50 65
                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
GlukrgAsnValVaiValThrGluGlyAspLeuLySLysValLeuAspGlyCysAlaPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 IleProAlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetGluleuMetSerAspSerAsnLeuSerAsnLeuVallleThrAspAlaSerSerleu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AsnGlyValAspLysLysLeuSerAlaGluValGluLysMetLeuValGlnLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaProAsnGluGlyIleGluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13884 CTCACTAGGTTCACTAATAAACTTAGAACGTTCGGTCGTACTTTCACTGAGGCTTACGTT
        CITY: Rochester

STATE: New York

CUNTRY: U.S.A.

ZIP: 14603

COMPUTER READABLE FORM:
MEDICX TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,993

FILING DATE:
CLASSIPICATION DATA:
APPLICATION NUMBER: US 60/C47,194

FILING DATE: 20-MAY-1997

ATTORNEY/AGENT INPORMATION:
NAME: Goldman, Michael L.
REFERENCE/DOCKET NUMBER: 19603/1631

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENTAL 15600 has a praire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-613-486-15 (1-198) x US-09-080-983-1 (1-15500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.56e-125
991.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                               : 15500 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-080-983-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . -t
(E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĎĎ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

ò Dp.

d

q

```
TITLE OF INVENTION: DNA Encoding Phage
TITLE OF INVENTION: Abortive Infection Protein
TITLE OF INVENTION: From Lactococcus
TITLE OF INVENTION: lactis, and Method of Use Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: lan C. McLeod
                                                                                                                                        APPLICANT: Sylvain Moineau, Barbara
APPLICANT: J. BOller, Peter A. Vandenbergh,
APPLICANT: Ebenezer R. Vedamuthu, Jeffrey I
APPLICANT: Kondo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quest 4.1-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: N/A IDENTIFICATION METHOD: sequencing OTHER INFORMATION: DNA encoding phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: phage abortive infection LOCATION: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Acer
OPERATING SYSTEM: MS-DOS (version SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/565,907A
FILING DATE: December 1, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 Kb storage
                                                                      Sequence 1, Application US/08565907A Patent No. 5814499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  December 1, 1995
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESCRIPTION: Genomic DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE: WI
DEVELOPMENTAL STAGE: N
HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: bacterium
CELL LINE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: genomic
CLONE: SMQ-20
POSITION IN GENOME: N/A
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 4467
TYPE: Nucleotide
STRANDEDNESS: Single
TOPCLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
FRAGMENT TYPE: N/A
CRIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                            Michigan
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANELLE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Mi
                                                                                                                                                                                                                                                             Sequence 1531, Application US/C9252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMCNAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMCNAS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/C74,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR SEQIEN NUMBER: US 60/094,190
PRIOR SEQIEN NOS: 33142
LENGTH: 2034
14004 ATTCCAGCTGANGATICGTACTINGCIGCAGATITICTGGGTACTIGCCGGANGCTCTCT 14363
                                                                             161 GluLeuGinGlnSerArgLysMetPheAlaSerMetTyrAlaLeuJysThrGluGlyGly 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 IleAlaTyrLysHisLysLeuProGlnLeuAsnAlaAla---AlaGluLeuGlyIlePro 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         654 ----CICGAAGCGCTTGAGCICGACGCCCAGGCGTTTCAGCAGGIGITTGGCGTCTTCGCT 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         597 ATAGAGGCGTTCGGCGATTGCAGCGACTCGCTGCCGCTAGCCGAGGATAGTGCGCCC 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 AlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeu 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     537 GCCGGCCTGGAATTCGTTGCGCTTGGCATGGCCGCGAAGTCGTCGTGGTTCTCGATGAC 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            864 GATGAGCGCCTCCCGGTCTTCGCGGCTCAGCGGGAAGTCGCCGATGAAGGCGCGCAGGA 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 ValValValThrGluGlyAspletLysLysValLetAspGlyCysAlaProLetThrArg 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 PheThrAshlysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCys 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 ProtysValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGlyGluArgAsn 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 AspLysLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAlaProAsn 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 GluGlyIleGluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSer 63
                                                                                                                                     163 GinGlnSerArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGly 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477 CAGGATGCGCGCCGC-----GGGGTGCCGTTCGCGATAGAACCAGGCGGCGGC 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-613-486-15 (1-198) x US-09-252-991A-1531 (1-2034)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.00
43.04%
22.15%
9.68%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                        US-09-252-991A-1531/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
```

D2.

ò

ò ď ò CC ò d

ò

Sp. ò ò

ò 55

ò 쇰 ò 유 à Ω. 3 op. ò

```
PRIOR APPLICATION DATA.
APPLICATION NUMBER: 08/565,907
ELING DATE: December 1, 1995
ATTORNEY AGENT INFORMATION:
NAME: IAN C MCLeed
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: 20,931
REFERENCE/TON INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: (517) 347-4103
TELEFAN: (517) 347-4103
TELEFAN: (517) 347-4103
TELEFAN: (517) 347-4103
TELEFA: No. 5910571e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENDET: NO. 5100571e
TENDET: NO. 5100571e
TENDET: NO. 5100571e
TENDET: NO. 5100571e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jength:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION METHOD: sequencing CTHER INFORMATION: DNA encoding phage OTHER INFORMATION: resistance PUBLICATION INFORMATION: N/A US-08-910-551B-1
                       UMBER: US/08/910,551B
August 11, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: phage abortive infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4467
TYPE: Nuclectide
STRANDEDNESS: Single
TOPOLOGY: Linear
XOLECULE TYPE:
DESCRIPTION: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.00
41.89%
24.32%
8.58%
      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISCLATE: WI
DEVELOPMENTAL STAGE: N
HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: bacterium
CELL TYPE: bacterium
                       APPLICATION NUMBER:
FILING DATE: August
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANELDE: N/A
IMMEDIATE SOURCE:
LIBRARY: genomic
CLONE: SMO-20
POSITION IN GENOME: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            %
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ω.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2239 TITATAGAITATIGIGIGAATGAAGAACATTTAGGGAATAAGGGAGCTATAAAATGIATT 2298
                                                                                                                                                                                                                                                                                                                            2:19 AAAACGAAAGTTGACAATTTCCCGTTTGTTGATAAATCGAGTAAATGGGATATTTTTTCT 2173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2179 TITITIGAAATATTACTICAACTAATTCCAAGGAGAGAGTGGATTAAAGAAATAAGGAAT 2238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspleulystysValLeuAspGlyCysAlaProLeuThrArgPheThrAsnLysLeuArg 109
                                                                                                                                                                                                                                                                                             GluLeuMetSerAspSerAsnieu------SerAsnieuValileThrAsp--- 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 PheGlyLeubeuLeuTyrAlaLeuAlaAlaArgThrThrSerPropysValGlnArgAla 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 AspSerAspValllePheSerAsnSerPheGlyGluArgAsnValValValThrGluGly 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 ------LysLeuberneuAsnGlyValAspLys-----LysLeubeuAerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2299 TTCCCAGTTATA-------ACAATACATTGAAAAAAAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 GluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGly---IleSluValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sylvain Moineau, Barbara
APPLICANT: J. Holler, Peter A. Vandenbergh,
APPLICANT: Ebenezer R. Vedamuthu, Jeffrey K.
APPLICANT: Kondo
TITLE OF INVENTION: DNA Encoding Phage
TITLE OF INVENTION: Abortive Infection Protein
TITLE OF INVENTION: From Lactococcus
TITLE OF INVENTION: lactis, and Method of Use Thereof
NUMBER OF SECURORS: 2
CORRESPONDENCE ADDRESS:
                                                                                                        4467
36
26
46
40
                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                  JS-09-613-486-15 (1-198) x JS-08-565-907A-1 (1-4467)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2455 ACTITCTTIGAAATATTAATGAA 2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Acer
OPERATING SYSTEM: MS-DCS (version
SOFTWARE: Wordperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 ThrehedlyArgThrPheThrGlu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 48864
CCMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-910-551B-1; Sequence 1, Application US/08910551B; Patent No. 5910571
    resistance
N: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Ckemos
STATE: Michigan
                                                                                                      0.466
85.00
41.89%
24.32%
8.58%
; OTHER INFORMATION: res; PUBLICATION INFORMATION: CS-08-565-907A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Michigan
: USA
                                                                                                                          Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
```

g

ò a 8

```
2179 TITTTIGAAAATATTACTTCAACTAATTCCAACGACAAGIGGATTAAAGAAATAAGCAAT 2238
                                                                                                                                                                                                                                                                                 2059 GAATTITTAAATGAATTTAATCTAATCTGTCGAGAAAATAACTTAATTATTAATGATAAT 2118
                                                                                                                                                                                                                                                                                                                                                                                                 2119 AAAACGAAAGTTGACAATTTCCCGTTTGTTGATAAATCGAGTAAATCGGATATTTTTCT 2178
                                                                                                                                                                                                                            2 GluleuMetSerAspSerAsnLeu-------SerAsnLeuVallleThrAsp--- 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 -------AlaSerSerLeuAsnGlyValAspiys-----LysLeuSerAla 30
                                                                                                                                                                                                                                                                                                                                         16
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                    US-09-613-486-15 (1-198) x US-08-910-551B-1 (1-4467)
```

S C

ರ್ಗ

ò

뎐 ò g ò g

ò

```
Sequence 13408, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2119 AAAACGAAAGTTGACAATTTCCCGTTTGTTGATAAATCGAGTAAATCGGATATTTTTTCT 2178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2179 TTTTTTGAAAATATTACTTCAACTAATTCCAACGACAAGTGGATTAAAGAAATAAGCAAT 2238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2338 GATACTAAAAATATA---GACAATATCTTTTCGAAAAGAAACATGGTTACCAATTTTAAT 2394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2395 GTTTTCGAAAAATATTAGATTTATCATTAAAAGATTCAAGATTAACTAATAAGTTTTG 2454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 AspleuLysLysValleuAspGlyCysAlaProLeuThrArgPheThrAsnLysLeuArg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 PheGlyLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysValGlnArgAla 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 AspSerAspValIlePheSerAsnSerPheGlyGluArgAsnValValValThrSluGly 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---SerAsnLeuVallleThrAsp---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 ------AlaSerSerLeuAsnGlyValAspLys-----uysLeuLeuSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3. GluValGluLysMetLeuValGlnLysGlyAlaProAsnGluGly---IleGluValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2239 TTTATAGATTATTGTGTGAATGAAGAACATTTAGGGAATAAGGGAGCTATAAAATGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-613-486-15 (1-198) x US-08-909-425A-1 (1-4467)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD: sequencing
OTHER INFORMATION: DNA encoding phage
OTHER INFORMATION: resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2455 ACTITICALAMIATATICA 2478
                                                                                                                                                                                                                                                                                       NAME/KEY: phage abortive infection LOCATION: N/A IDENTIFICATION METHOD: sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 ------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 ThrPheGlyArgThrPheThrGlu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GluieuMetSerAspSerAsnLeu-
                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION: N/A
                                                                                                                                               ORGANELLE: N/A
ORGANELLE: N/A
IMMEDIATE SOURCE:
L'ERRAY: genomic
CLONE: SMQ-20
POSITION IN GENOME: N/A
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.466
85.00
41.89%
24.32%
8.58%
                                        DEVELCE:...
BAPLOTYPE: N/A
TISSUE TYPE: N/A
TISSUE TYPE: Dacterium
                           INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-252-991A-13408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-909-425A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          음
2239 TITAINGATTATTGIGTGAATGAAGAACAITTAGGGAATAAGGGAGCIATAAAATGIAIT 2298
                                                                                          -----ACAAATACATTGAAACAAAAAAAGTA 2337
                                                                                                                                                               2395 GTTTTCGAAAAATATTAGATTATCATTAAAAGATTCAAGATTAACTAATAAGTTTTTG 2454
                                                                                                                                                                                                                   90 AspLeuLysLysValLeuAspGlyCysAlaProLeuThrArgPheThrAsnLysLeuArg 109
                                           50 PheGlybeureuLeuTyrAlabeuAlaAlahrgThrThrSerProbysValGlrArgAla 69
                                                                                                                                 70 AspSerAspValIlePheSerAsnSerPheGlyGluArgAsnValValValThrGluGly 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sylvain Moineau, Barbara
APPLICANT: J. Holler, Peter A. Vandenbergh,
APPLICANT: Benezer R. Vedamuthu, Jeffrey K.
APPLICANT: Ebenezer R. Vedamuthu, Jeffrey K.
TITLE OF INVENTION: DNA Encoding Phage
TITLE OF INVENTION: Abortive Infection Protein
TITLE OF INVENTION: Abortive Infection Protein
TITLE OF INVENTION: Abortive Infection Protein
TITLE OF INVENTION: 1actis, and Method of Use Thereof
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                2455 ACTITCTTTGAAAATATTAATGAA 2478
                                                                                                                                                                                                                                                                                                         110 ThrPheGlyArgThrPheThrGlu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Acer
OPERATING SYSTEM: MS-DOS (version
SOFTWARE: Wordperfect 5.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/909,425A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: August 11, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/565,907
FILING DATE: December 1, 1995
ATTONNEY/AGGNT INFORMATION:
NAME: 1an C. McLeod
REGISTRATION NUMBER: 20,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08909425A
Patent No. 5928688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (5.7) 347-4100
TELEFAX: (5.7) 347-4101
TELEFAX: No. 5926888
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S: Single
Linear
                                                                                      2299 TTCCCAGTTATA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 4467
Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: N/A ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: Mchigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Ckemos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-909-425A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
```

Φ

us-09-613-486-15.rni

```
Sequence 13950, Application US/09252991A

Sequence 13950, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: March Carl Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFREENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PR.OR APPLICATION NUMBER: US 60/074,788

PR.OR APPLICATION NUMBER: US 60/094,190

PR.OR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 13950

LENGTH: 2433
                                                                                                                                                                            17 AlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGluValGluLysMetLeu 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AlaSerSerLeuAsnGlyValAsplysLysLeuLeuSerAlaGluValGluLysMetLeu 36
                                                                                                                                                                                                             130 GCCAACACCATGAACGGTGTCTACCGCGAGGCGATGGCGAAGACCATCGCACGGCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 GGATCCTCGAACTCAAGGGCCAACTGCGGCCTGGAGACCCTCGGCAAGCCGGTGGTC
                                                                                                                                                                                                                                                                                                                                   57 LeuAlaAlaArgThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 -------AACGAGCTGATCAAGGTCACGACGCCGACGCCCGGCCTTCTACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyCysAlaProLeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --ValAspPheCysIleAlaTyrLysHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 GCCGCGATCAACGGCGCTGCGCTGGGCGGCGGCTGGGAGATCTGCCTGGCTGCCACCAC
                                                                                                                                                                                                                                                        37 ValGlnLysGlyAlaProAsnGluGlyIleGluValValPheGlyLeuleuTyrAla
                                                                                                                                                                                                                                                                                            190 GCGGAGAAA------GAGGGATCGCC------GGCGTGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                            77 AsnSerPheGlyGluArgAsnValValValThrGluGlyAspLeuLysLysValLeuAsp
                                                                                                                                                                                                                                                                                                                                                                       223 -----ACCTCGGCSAAGACCTTCTTCGCCGGCGGCGATCTC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 LysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIlePro 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 GGCATCGCCCTGGACAATCCCGGCGTGCAGCTCGGCCTGCCG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2433
30
26
50
28
5
    2199
30
26
26
28
3
                                                                                                                                        US-09-613-486-15 (1-198) x US-09-252-991A-13503 (1-2199)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-09-613-486-15 (1-198) x US-09-252-991A-13950 (1-2433)
                      Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CRGANISM: Pseudomonas aeruginosa
    0.557
81.00
41.79%
22.39%
8.17%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.00
41.79%
22.39%
8.17%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 GluAlaTyr-
                        Score:
Percent Similarity:
Best Local Similarity:
Cuery Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-13950/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-252-991A-13950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
                                                                                                                                                                                                               QC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                          ò
                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 GCGGAGAAA------GAGGGGATCGCC-----GGCGTGCTG----- 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ValAspPneCysIleAlaTyrLysHis 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 GCCGCGATCAACGGCGCTGCGCTGGGCGGCGGCTGGGAGATCTGCCTGGCCTGCCACCAC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 decarecresaacreaassecaacresessecrissaacecresaceressaassessessesses 307
                                                                                                                                                                                                                                                                                                                                                                                                                            17 AlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGluValGluLysMetLeu 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 ValGlnLysGlyAlaProAsnGluGlyIleGluValValPheGlyLeuLeuLeuTyrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 LeuAlaAlaArgThrThrSerProLysValGlrArgAlaAspSerAspValllePheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 ------ACCTCGGCGAAGAGCCTTCTTCGCCGGCGGCGATCTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 Asr.SerPheGlyGluArgAsnValValValThrGluG.yAspLeuLysLysValLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 GlyCysAlaProLeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIlePro 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 CGCATCGCCCTGGACAATCCCGGCGTGCAGCTCGGCCTGCCG 439
                                                                                                                                                                                                                                                                                                                                                                                        US-09-613-486-15 (1-198) x US-09-252-991A-13408 (1-1743)
                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                     Gaps:
                PRIOR APPLICATION NUMBER: US 60/574,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/594,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEC 1D NOS: 33142
SEC ID NO 13408
LENGTH: 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                      TYPE: DNA CREADONAS AETUGINOSA US-09-252-991A-13408
1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 GluAlaTyr------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13503
                                                                                                                                                                                                                                                   0.389
81.00
41.79%
22.39%
8.17%
  CURRENT FILING DATE:
                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
```

200 -----

g

ઠે 셤 ö Dp ò a

ò

d

DB:

ò

G G ਨੇ a ò 129

303

429

222

261 26

96

2328 GCCAACATGAACGGTGTCTACCGCGAGGGATGGCGAAGACCATCGCACGGCTGGAG 2269

US-39-252-991A-13503 Alignment Scores

LENGTH: 2199

us-09-613-486-15.rni

Best Local Similarity: 20.98% Mismatches: 60 Query Match: 7.97% Indels: 62 D5: 2	-09-613-486-15 (1-198) x US-08-770-544-15 (1-1434)	Cy 12 LeuVallieThraspalaSerSerieuAsnGlyValAspLysLysLeuLeuSerAiaGlu 31 	Gy 32 ValGluLysMetLeuValGlnLysGlyAlaProAsnGluGlylleGlu 47	::: ::::::::::::::::::::::::::::::::::	Oy 48 ValValPheGlyLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysValGln. 67 :::	1000 ATMINISTRATOR TO THE TOTAL TRANSPORTING TO THE TRANSPORT TO THE TRANS	Db 1060 GACGGGTATAGGGTGGAGACCGAATTAGGTCAAAAGAGAGTC 1101	Oy 85 ValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaPro 100 ::::::::::::::::::::::::::::::::::	LeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrVal	Db 1162ACCAACACTGTGCGATCCTTCATGAGGTATTTTGCTCACACCACTATT 1209	Cy :21 AspthcyslealaryrLysHisLysheuproGluLeuAsnAlaAladlaLeuG;y 140		1267 GTCCCGAAGAGGTTCACTCCGTACTGCTTCGACTTCGCACTACTGGATAACAGATATTAC	Cy 149 AlaAlaAspPheLeuGlyThrCysProLysLeuSerGlubeuGlnGlnSerArgLysMet 168	Db 1327 CCGGCGGACGTGTTGAAGGCTAACGCA 1353	Cy 169 PheAlaSerMetTyrAlaLeuLysThrGluGiyGlyValValAsmThrPrcValSerAsn 188		Cy 189 LeuArgGInLeuGly 193		RESULT 11	GEN	AFFLICANT: GOUSTIVES, DELLIES LING, Kai-Shu TITE OF INVENTION: GRAPEVINE IRAFROIL	NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS: ADDRESSEE: Nixon, Hardrave, Devans	SIREET: Clinton Square, P.O. Box 1051 CITY: Rochester			7	SOFIWAKE: CURRENT APPLICE
Qy 37 ValGlniysGlyAlaPrcAsnSluGlyIleGluValValPheGlyLeubeuLeuTyrAla 56 	57 LeualaalaataghrThrSerProtysValGlnArgAlaaspSerAspValllePheSer 7	Db 2235 2197 Qy 77 AsnSerPheGlyGluArgAsnValValValThrGluGlyAspLeuLysLysValLeuAsp 96	Db 2196AACGAGCTGATCAAGGTCACCAAGGCCGACCCCGGCCTTCTACCAG 2149	97 GlyCysalaProLeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThr 116	Db 2148 GGCATCCTCGAACTCAAGGGCCAACTGCGGGCCTGGAGACCCTCGGCAAGCCGGTGGTC 2089 Ov 117 GlualaTvr	2088 GCCGCGATCAACGCGCTGCGCTGGGCGGCGGGGGGGGGG		2028 SULT 10	()		APPLICANT: Ling, Kai-Shu , TILLE OF INVENTION: GRAPHINE LEAFROLL VIRUS PROTEINS AND TITLE OF INVENTION: THEIR PIECE	NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS		CITY: Rochester CITY: Rochester CITY: Pow York	COUNTRY: U.S.A.	, COMPUTER READABLE FORM: , MEDIUM TYPE: Floppy disk	COMPUTER: IEM FC compatible OPERATING SYSTEM: PC-DGS/MS-DCS	SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:	APPLICATION NUMBER: US/08/770,544; FILING DATE:				INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:	LENGTH: 1434 base pa TYPE: nucleic acid	STRANDE	, MOLECOLE 17FE: CDNA US-08-770-544-15	Alignment Scores: 0.543 Length: 1434 Pred. No.: 0.540 Matches: 434	40.49% Conservative:

```
Alignment Scores:
Pred. No.:
                                                                 RESULT 12
US-09-214-808-1
   189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \dot{\varsigma}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ω.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1000 ATASTGGCCATGATACAACTTTTCGTACTCTACTGTAAAGAATATAAGCGTCAAA 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1267 GTCCCGAAGAGGTTCACTCCGTACTGGTTCGACTTCGCACTACTGGATAACAGATATTAC 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :::|||
----GCTAAT 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1102 TACTTAAGTTATTCGGAAGTAAGGSAAGCTATATTAGGAGGAAATACGGTGCGTCTCCA 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .213 ACTCTACTATAGAGAAGAAATTCAG---CCAGCGTGTACTGCCCTAGCTAAGCACGGC 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- AAGGCTAACGCA 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 ValValThrGluGlyAspLeuLysLysValLeu------AspGlyCysAlaPro 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 LeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AspPheCysIleAlaTyrLysHisLysLeuProGlnLeuAsnAlaAlaGluLeuGly 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------AlaGluAspSerTyrLeu 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 AlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSerArgLysMet 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 PheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrProValSerAsn 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------GCAAGA 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 ValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysValGlm 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 -----ArgalaAspSerAspValllePheSerAsnSerPheGlyGluArgAsnVal 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuvalileThrAspAlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGlu 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 ValGluLysMetLeuValGlnLysGly-----AlaProAsnGlu---GlylleGlu 47
                                                                                                                                                                                                                                                                                                                                                                                   443
443
660
62
11
                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-09-613-486-15 (1-198) x US-09-579-259-15 (1-1434)
                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6000008
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/621
TELECOMMINICATION INFORMATION:
TELEPHONE: (716) 263-1804
TELEPHONE: (716) 263-1804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 904 TIGCCGATAACGGAAGCICTACAGATAAAC----
APPLICATION NUMBER: US/09/579,259
                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .354 ATGGCTTGCGCTATAGCGATTAAATCA--
             FILING DATE: 25-May-2000
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1434 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .327 cceeceakcererra----
                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                     0.543
79.00
40.49%
20.98%
7.97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 IlePro----
                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                     US-09-579-259-15
                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ДQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ਨ
```

314743 ---GGAACCGGCAAAAAACTTCTGGCACGGGGTATTCATGAAGCTGCCAGACGTTCCGGC 314799 314800 AGCAAGCTCATCAGCTCAGAAGACGCAAGTGGGGAATCGCTTTTTGGCTTCGCCCCGAGC 314859 314860 GAGGGCGCCAGGAAGGTGCTTGGCCTACTCCCAATACCATCCCAAAGCAACCTGCTGATC 314919 314962 ATAGAAGTCATCGAGACAGGGGCTTATCGGCGCCTGGGGGACAAC-----GAGAGAGGG 315015 315034 ATCCTGGCATCGACGCGCCCCTTCCTGAGTTGGGCTCGAGCTGGGCAGCTG---ATACCT 315090 -----CAGGAACGTCTG 314961 Sequence 1, Application US/09214808A

Patent No. 6475793

GENERAL INFORMATION:
APPLICANT: Resenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Broughton, William John
ITILE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
Patent No. 6475793

ITILE OF INVENTION: Plasmid
File RefereNce: CARPO68
CURRENT FILING DATE: 1999-66-22
FRIOR APPLICATION NUMBER: US/09/214,808A
CURRENT FILING DATE: 1997-07-10
FRIOR FILING DATE: 1997-07-10
FRIOR FILING DATE: 1997-07-10
FRIOR FILING DATE: 1997-07-10
FRIOR FILING DATE: 1997-07-10 ValValValThrGlu---GlyAspleuLysiysValLeuAspGlyCysAlaProLeuThr 102 123 CyslleAlaTyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIlePro 142 ---AlaAspPheLeu 153 41 ------AlaProAsm 43 64 ProLysvalGlnArgAlaAspSerAspValIlePheSerAsnSerPheGlyGluArgAsn 83 1 MetGluLeuMetSerAspSerAsnLeuSerAsnLeuValIleThrAspAlaSerSerLeu 20 44 GluGlyIleGluValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSer 63 314692 ATCGABABAGCTTGCCGCTTCTACTCCCCGGTCATGATTACCGGACAAGCC------21 AsnGlyValAspLysLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGly 103 ArgPheThrAsnLysJeuArgThrPheGlyArgThrPheThrGluAlaTyrVaiAspPhe 314920 GAGAGCGTCGAATGCCTGTGCGTCGACGCT------Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-613-486-15 (1-198) x US-09-214-808-1 (1-536165) 315016 CGGTTCGAAGGCCGCCTG------143 AlaGluAspSerTyrLeuAla-1401 LeuArgGlnLeuGly 193 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1 LENGTH: 536165 5.2e+03 79.00 38.27% 26.02% 7.97% 1387 TTAAGGCGTAAAGGT TYPE: DNA CRGANISM: Rhizobium US-09-214-808-1 Percent Similarity: Best Local Similarity: Query Match:

us-09-613-486-15.rni

g ò g

```
CS-09-252-991A-3636/C
Sequence 3636, Application US/C9252991A
Sequence 3636, Application US/C9252991A
Sequence 3636, Application US/C9252991A
PAPPLICANY:
MAYCO TO RUBERION:
MAYCO TIME OF INVENTION:
MAYCO TIME OF INVENTION:
MERCO MERCO MERCO TIME OF INVENTION OF INVENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          859 ACCEGGTTGATCAGCGCTCCTGCCAGCAGCCTGGAGAACCTCGTGCTGCTGCGGATCATG 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 924 ACCGCCCTGTTGACTCGCTACACGCTCGTCGCCAGGACCTGCCGCGACAGATCGAAGTC 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  864 SCCGAGCTGCCTCCGTGGGGGAAGTGGTGCGCGGCCTCGACAACGGCGAGTTCGAAGCC 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 TACTACCAGCCCAAGGTGGCCCTGGATGGCGCCGCGCGCCGAGGTCCTGGCA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------GlyCysAlaProLeuThrArgPheThrAsnLysLeuArg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 CGCTGGAACCACCCGCATCTCGGCGTATTGCCGCCGTCGCATTTCCTCTTATGTGAA 685
                                                                                                                                                                                                                        Glu-----LeuGlnGlnSerArgLysMetPheAlaSerMetTyrAlaLeuLysThrGlu 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 TGCCTGGGCCTCAATTTTCTCGGCGACCTTGGCAAGCCA---TTCAGCCTGGAGCGGATC 925
                                          143 AlaGluAspSerTyrLeuAlaAlaAspPheLeu-----GlyThrCysProLysLeuSer 160
                                                                                                                          754 Grecardetricionacrigionregio and reconstruction of the contraction of the contraction
                                                                                                                                                                                                                                                                                                             814 GASITCCACCTGCCGCCCAGTTCGGTGATGTTCGAGATC--------ACCGAG 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ArgAsnValValValThrGiuGlyAspLeu-----LysLysValLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 PheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLys---ValGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                  179 GlyGlyValValAsnThrProValSerAsnLeuArgGlnLeuGlyArgArgSluValMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 AlaAsp-----SerAspValllePheSerAsnSerPheGlyGlu-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerAsnLeuSerAsnLeuVallleThrAspAlaSerSerLeuAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 LysLeuleuSerAlaGluValGluLysMetLeuValGlnLys----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-613-486-15 (1-198) x US-09-252-991A-3636 (1-1491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA CRGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.931
77.50
37.92%
25.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-252-991A-3636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                             161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  င္ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                   CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                            CD.
                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TO PSEUDOMCNAS
315091 GCTCTTGAGTCGCGTCTCGCGCCGGGTCACGTCTTTCTTCCCCCTCTATGCGATCGCCTC 315150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 TSCCTGGGCCTCAATTTTCTCGGCGACCTTGGCAAGCCA---TTCAGCCTGGAGCGGATC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GlyCysAlaProLeuThrArgPheThrAsnLysLeuArg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     589 CGCTGGAACCACCCGCATCTCGSCGTATTGCCGCCGTCGCATTTCCTCTATGTSATGSAA 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---PheGlyArgThrPheThrGluAlaTyrValAspPhe 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 CyslleAlaTyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyllePro 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 ACCGCCCTGTTGACTCGCTACAACGCTCGCCAGGACCTGCCGCGACAGATCGAAGTC 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  697 --- CTGGCGACGCGCAGAAGCTGGCGCAGTTGGGGCAGCCGATCAACCTGGCGTTCAAC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 AGCGGCATGGACGGCCTGGCGTTCCTTCGCCACGCAAGCCTGAGCGGCAAGGTCCATTCG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 GIGAICCICAGCAGCGAGGIGGAICCCAICCIGCGCCAGGCCACCAIIICGAIGAICGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------GlyAlaProAsnGluGlyIleGluValVal 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheGlybeubeuTyralabeuAlaArgThrThrSerProbys---ValGlnArg 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- ArgAsnValValValThrGluGlyAspLeu-----LysLysValLeuAsp 96
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SECUENCES RELATING TO PY
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SECUENCES RELATING TO PY
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REBERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3735
LENGTH: 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerAsnLeuSerAsnLeuValIleThrAspAlaSerSerLeuAsnGly---ValAspLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaAsp-----SerAspVal1lePheSerAsnSerPheGlyGlu-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649 ACCTACAACCTGGTCGACAAGCTGTTCTGGCAACTGTTCAGCCAGGGG------
                                                                                                                                        154 GlyThrCysProLysLeuSerGlu-----LeuGlnGlnSerArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysLeuLeuSerAlaGluValGluLysMetLeuValGlnLys----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-613-486-15 (1-198) x US-09-252-991A-3735 (1-1233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                             US-09-252-991A-3735
; Sequence 3735, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.694
77.50
37.92%
25.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 Thr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
```

ठे S ેં a δö Dic. ò a ò q ò Cp $\dot{\delta}$ 엄

ò q ò

us-09-613-486-15.rni

```
110 Thr -----
                                                                                                                                                                                                                                                                                                                 161
                                            8
                                                                                                        3 8 3
                                                                                                                                                                                                       යි රු සි
                                                                                                                                                                                                                                                                                                        8 8 8
                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION MARKED TO RUBERFIELD ET al.

TITLE OF INVENTION: NUCLETC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PEDIGATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PELICATION NUMBER: US 60/074,786
PRIOR PELICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ 1D NOS: 33142
LENGTH: 4884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 TGCCTGGGCCTCAATTTTCTCGGCGACCTTGGGAAGCGA---TCAGGCTGGAGCGGATC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 ACCGCCCTGTTGACTCGCTACAACGCTCGTCGCCAGGACCTGCCGCGACAGATCGAAGTC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 GCCGAGCTGCCCTCCGTGGCGGACGTGGTGCGCCCTCGACAACGGCGGAGTTCGAAGCC 439
                                                                                                                                                                                                                                                                 179 GlyGlyValValAsnThrProValSerAsnLeuArgGlnLeuGlyArgArgGluValMet 198
                                                                                                                                                                                                                                                                                      Glu-----LeuGlnGlnSerArgiysMetPheAlaSerMetTyrAlaLeuLysThrGlu 178
                                                                 123 CyslleAlaTyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIlePro 142
                                                                                                                                143 AlaGluAspSerTyrLeuAlaAlaAspPheLeu-----GlyThrCysProLysLeuSer 160
                                                                                                                                                              579 GICCAICCIICGCAACIGGGIICGCGIGCCIGGCCGAGAACAICICGGGGGIIGCIGACC 520
                                                                                                                                                                                                                                 519 GAGTTCCACCTGCCGCCCAGTTCGGTGATGTTCGAGATC------ACCGAG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerAsnieuSerAsnLeuVallleThrAspAlaSerSerLeuAsnGly---ValAspLys 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 ---------GlyAlaProAsnGluGlyIleGluValVal 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 PheGlyLeuLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLys---ValGlnArg 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 AlaAsp-----SerAspValilePheSerAsnSerPheGlyGlu----- 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ArgAsnValValValThrGluGlyAspLeu-----LysLysValLeuAsp 96
                                                                                                 ---craccancecechaeaadcraccecharraceceancancancraccroscerranc
PheGlyArgInrPheThrGluAlaTyrValAspPhe
                          684 ACCTACAACCTGGTCGACAAGCTGTTCTGGCAACTGTTCAGCCAGGGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 LysLeuLeuSerAlaGluValGluLysMetLeuValGlnLys--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4884
60
31
90
59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-613-486-15 (1-198) x US-09-252-991A-3824 (1-4884)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-3824
; Sequence 3824, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.84
77.50
37.92%
25.00%
7.82%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-C9-252-991A-3824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
                                                                                                  989
                                                                                                                                                                                                   161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ें
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ω̈́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                ò
                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                                   20
                                 Dp.
                                                                 ò
                                                                                               a
                                                                                                                                ठे
                                                                                                                                                             a
                                                                                                                                                                                                                                                                   ò
 ે
```

```
607
                                                                                                                                                                                                                                                                                                                                                                                                                         142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glu------beuGlnGlnSerArgLysMetPheAlaSerMetTyrAlaLeuLysThrGlu 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 SlyGlyValValAsnThrProValSerAsnLeuArgGlnLeuGlyArgArgGluValMet 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                770 ACCEGETTARTCAGCECTCCTGCCAGCAGCCTCGAGAAACCTCGTGCGTCTGCGGATCATG 829
440 IACTACCAGCCCAAGGTGGCCCTGGATGGCGGCGGCGCGGCGCCGAGGTCGCGA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    665 greenrechiedenachdenredenredentesechdenenantresechtschen 724
                                                                                                                 -----GlyCysAlaProLeuThrArgPheThrAsnLysLeuArg
                                                                                                                                                                                                                                                                           -------PheGlyArgThrPheThrGluAlaTyrValAspPhe
                                                                                                                                                                                                                                                                                                                                                                                                                         123 CysileAlaTyrLysHisLysLeuProSinLeuAsnAlaAlaAlaGluLeuGlyIlePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  608 ---CTGGCGACGCGCAGGAAGCTGGCGCAGTTGGGGCCGATCAACCTGGCGTTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 AlaGluAspSerTyrLeuAlaAlaAspPheLeu-----GlyThrCysPrcLysLeuSer
                                                                                                                                                                                          soo cecreeaaccacceccarcreecantrecceccarcearricerenararanseaa
                                                                                                                                                                                                                                                                                                                                            560 ACCTACAACCTGGTCGACAAGCTGTTCTGGCAACTGTTCAGCCAGGGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              725 sagriccaccigcccccagriccgroardricgagaic-----
```

Search completed: November 8, 2003, 01:42:06

Run on:

```
Sequence 1, Apply Sequence 12, Apply Sequence 124, App Sequence 1292, App Sequence 119, Apply Sequence 119, Apply Sequence 119, App Sequence 575, App Sequence 575, App Sequence 129, App Sequence 129, App Sequence 6518, App Sequence 6518, Apply Sequence 1, Appli Sequence 1222, Appli Sequence 1222, Appli Sequence 1197, Appli Appli Sequence 1197, Appli Appli Sequence 1197, Appli Ap
                        Sequence 15, Appl
Sequence 15, Appl
Sequence 22, Appl
Sequence 1, Appl
Sequence 5760, Ap
Sequence 6808, Ap
Sequence 4239, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6333, Ap
2237, Ap
7237, Ap
1237, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1237,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5,
Sequence 63
Sequence 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYMBIONT OF APHIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 US-10-135-696-3

1 US-09-976-451-1

9 US-09-976-451-1

10 US-09-976-451-10

10 US-09-974-300-127

10 US-09-974-300-1197

10 US-09-974-300-1197

10 US-09-974-300-1197

10 US-10-974-300-1308

12 US-10-087-402-5

12 US-10-128-714-7237

4 US-10-128-714-7237

4 US-10-128-714-6237

1 US-10-128-714-6237

US-10-128-714-6237

US-10-128-714-6237

US-10-128-714-6237

US-10-128-714-6237
GENERAL INFORMATION:
APPLICANT: BHIGENOBU, SHUJI
APPLICANT: HATARABE, HIDENI
APPLICANT: HATARIA MASAHIRA
APPLICANT: HATORI, MASAHIRA
APPLICANT: GENOME DIA OF BACTERIAL SYM
ITLE DE INVENTION: GENOME DIA OF BACTERIAL SYM
FILE REFERENCE: 081356/0159
CURRENT FILING DATE: 2001-02-23
PRICR APPLICATION NUMBER: US/99/790,988
CURRENT FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIN OF ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09790988
Patent No. US20020127687A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.46e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1455 1
5964 1
49136 1
59065 1
                                                                                                                                                                       1068
8095
                                                                                                                                                                                                                                                                                                                                      81940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Buchnera
    LENGTH: 640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                    US-09-790-988-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.5
73.5
73.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
       Command line parameters:
-MODEL=frame+ p2n.mcdel -DEV=xlh
-MODEL=frame+ p2n.mcdel -DEV=xlh
-MODEL=frame+ p2n.mcdel -DEV=xlh
-Wolst=frame+ p2n.mcdel -DEV=xlh
-DES=ublished Applications NA -OFMT=fastap -SUFFTx=mpb -MINMATCH=0.1
-DOPCLE -DOPEXT=0 -UNITS=bits -STAT=1 -END=-1 -XATRIX=blosum62
-TRANS=humman40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAXIEN=10:
-TRANS=humman40.cdi -USTR=45 -DOCALIGN=200 -THR SCORE=pct -THR MAXIEN=10:
-TRANS=humman40.cdi -USTR=45 -DOCALIGN=200 -NGRM=ext -HBAPSTZE=500 -MINLEN=20:
-MAXIEN=200000000 -USR=US09613486 @CGN 1 1 221 @runat 0711203 120413 27179
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=1 -SARAPOP=10 -XGAPEXT=0.5
-EGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPE=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Appli
                                                                                                                                                                                      (without alignments)
2092.085 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                              I MELMSDSNLSNLVITDASSL.......GGVVNTPVSNLRQLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                  ; Search time 302 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications NA: 

| cgn2 6/prodata/2/pubpua/USG7 PUBCCXB seq: *
| cgn2_6/prodata/2/pubpua/PCT7 NEW PUB.seq: *
| cgn2_6/prodata/2/pubpua/PCT7 NEW PUB.seq: *
| cgn2_6/prodata/2/pubpua/USG6 PUBCCXB seq: *
| cgn2_6/prodata/2/pubpua/USG6 PUBCCXB seq: *
| cgn2_6/prodata/2/pubpua/USG7 NEW PUB.seq: *
| cgn2_6/prodata/2/pubpua/USG8 NEW PUB.seq: *
| cgn2_6/prodata/2/pubpua/USG8 NEW PUB.seq: *
| cgn2_6/prodata/2/pubpua/USG9 PUBCCXB.seq: *
| cgn2_6/prodata/2/pubpua/USG9 NEW PUB.seq: *
| cgn2_6/prodata/2/pubpna/USG9 NEW PUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/pubpna/US60_PUBCCMB.seg:*
                        GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
                                                                                                                OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2141354 segs, 1595478879 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.4 640681 10 US-09-790-988-1
                                                                                                                                                                  01:33:59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                   Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                  2003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length: 0
length: 200000000
                                                                                                                                                                                                                                                                 US-09-613-486-15
991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Score Match Length DB
                                                                                                                                                                  φ,
                                                                                                                                                                  November
                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.5
                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB Maximum DB 8
                                                                                                                                                                                                                                                                                                              Seguence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
```

Result Š. υ

```
Sequence 15, Application US/10138842A
PUDIcation No. US2030148390A1
GENERAL INFORMATION:
APPLICANT: GCNSALVES, DENNIS
APPLICANT: LING, KAI-SHU
TILLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
TITLE OF INVENTION: THEIR USES
                                                                                                                                                                                                                                                                                                                                                                       US-09-613-486-15 (1-198) x US-09-815-242-6624 (1-1356)
                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                           Indels:
  : SCFTWARE: FastSEQ for Windows Version 4.(
: SEQ ID NO 6624
: LENGTH: 1356
: TYPE: DNA
: CRGANISM: Enterococcus faecalis
: FEATURE:
: NAME/KES:
: LOCATION: (1) .. (1356)
: LOCATION: (1) .. (1356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          991 GGGGAATGCCG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            892 ACATTTGAAGAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            853 GAT-----
                                                                                                                                                                                                                               0.851
79.00
36.53
24.20
7.97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 SerSerLeu-
                                                                                                                                                                                                                                                                                        Similarity:
                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-138-842A-15
                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                           Query Match:
DB:
                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                                                                                                                             \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ω.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                               435915 AAAAATCAACGTSSATCATTAAGCATTGATGACGAAGGTACTCCAGGTCAAASAATATT 435856
                                                                                                                                                                                                                                                                       435795 GGTGTTAAGTCTACCGGAAATGGTCGTGGAATCTTATTCGTGTCTACCTATGCTCGT 435736
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------ACCTATATG 435719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TATGCTGTAAATTTTCTGGA------GGACAGGTAGATATTACT 435625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435624 TCCGGAAAATTTGTATTTTCTACTTCGGAAGCTTATTAATAAAAALTGGAAAAATTGTT 435565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleAlaTyriysHisiysLeuProGinLeuAsnAlaAlaAlaGluLeuGlyIleProAla 143
                                                                                                                                                                                                                                                                                                                              ----GiyCysAlaProLeuThrArg 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 GluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGln 163
                                                                                                                                                                                                                                                                                                                                                                                                           104 PheThrAshLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCys 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 GinSerArgiysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsn 183
                                                                                                                                                               LysValGinArgAlaAspSerAspValIlePheSerAsnSerPheGlyGluArgAsnVal 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435717 TTATCTGGAAAGTCTAAATTAGATGATATAATTAAAAGCGTCGACTATGGAATA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435564 ACACCAATTAAAAACACTACTCATAGGATCAGGATTAGAAGTTATG 435517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 ThrProValSerAsnLeuArgGlnLeuGlyArg---ArgGluValMet 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICAN: Xu, Howard

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: IDENTIFY, OUR ELITRA, OILA
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/20, 848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/200, 727
PRIOR APPLICATION NUMBER: 60/200, 727
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/202, 578
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR APPLICATION NUMBER: 60/245, 578
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
      32
26
53
53
53
                       Conservative:
Mismatches:
Indels:
                                                                                                                         US-09-613-486-15 (1-198) x US-09-790-988-1 (1-640681)
                                                                                                                                                                                                                                            ValvalThrGluGlyAspieuLysiysValieuAsp--
    Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6624, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-C2-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                   435735 ATGACTAAT--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
Wall, Daniel
Tradick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Haselbeck, Robert
83.50
37.18%
20.51%
8.43%
                                                                                                                                                                                                                                                                                                                            ------ 16
                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -09-815-242-6624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                 65
                                                                                                                                                                                                                                                85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qc
                                                                                                                                                                 ò
                                                                                                                                                                                                   d
                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                   D.
                                                                                                                                                                                                                                                                                                                                                                                                           ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                               DD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S<sub>C</sub>
```

```
---GGAATCTAT 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 G.yThrCysProLysLeuSerGluleuGlnGlnSerArgLysMetPheAlaSerMetTyr 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                748 GATTCAGAAGAGAAGTGATTGTCATTGCAACTAGAAATCCTGGTAAAGGGAAAGAGTTT 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     808 AGTICAAITITIGGIGAAAAAGGAIATACAGTI-------AAGACGITATIA 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 AspGlyCysAlaProLeuThrArgPheThrAsn-----LysLeuArgThrPheGlyArg 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 ThrPheThrGluAlaTyrValAspPheCysIleAlaTyrLysHisLysLeuProGlnLeu 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------AATGCTCGTCTAAAAGCTGAAACAATT 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         931 GCAGAAATTTTACAGAAACCAGTATTAGCAGATGATTCAGGATTAATTGTTGATGGGTTA 990
                                                                                                                                                                                                                                                                                                           1 MetGluLeuXetSerAspSerAsnLeuSer-----AsnLeuValleThrAspAla 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 SerAsnSerPheGlyGluArgAsnValValValThrGluGlyAspLeuLysLysValLeu 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .012 TCTGCTCGTTTTGCTGGTGAGCCAACTAACGATGCTTCAAATAATGCGAAACTACTA 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 AlaLeuLysThrGluGlyGlyValValAsnThrProValSerAsnLeuArgGinLeu 192
                                                                                                                                                                                                                                                                                                                                                 33 GlurysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPheGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AsnGlyValAspLysLysLeuLeuSerAlaGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            589 GGTGAATTTGTGGAAATTCAAGGAACGGGTGAAGAAGCTACCTTCTCAGGAGATGAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TATCCGAATITGCCAGATGTAGAAGAAACTGGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 AsnAlaAlaAlaGluLeuGly.leProAlaGluAspSerTyrLeuAlaA.aAspPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 ------LeuleuTyrAlaLeuAlaAlaArgThrThrSerProlysValGlnArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 AspSerAsp------Vallle------Phe
1356
53
27
73
66
```

891

153

648

25

69

75

```
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
92.
 RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \stackrel{>}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1267 GTCCCGAAGAGGTTCACTCCGTACTGCTTCGCACTACTGGATAACAGATATAC 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1060 GACGGGTATAGGGTGGAGACCGAATTA---------GGTCAAAAGAGAGTC 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1102 TACTIPAGITATICGGAAGIPAGGGAAGCTATATTAGGAGGAAATACGGTGCGTCTCCA 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---AAGGCTAACGCA 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 AlaAlaAspPheieuGlyThrCysProiysLeuSerGluLeuGinGlnSerArgLysMet 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 PheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrProValSerAsn 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 LeuThrArgPheThrAshLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- AlaGluAspSerTyrLeu 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 ValValThrGluGlyAspLeulysLysValLeu------AspGlyCysAlaPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GCAAGA 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 ValGluLysMetLeuValGlnLysGly------AlaProAsnGlu---GlyIleGlu 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 ValValPheGiyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysValGin 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuVallleThrAspAlaSerSerLeuAsnGlyValAspLysLeuLeuSerAlaGlu 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AspPheCysIleAlaTyrLysHisLysLeuProGinLeuAsnAlaAlaGluLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GCTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 ------ArgAlaAspSerAspValllePheSerAsnSerPheGlyGluArgAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1162 ...-----ACCAACACTGTGCGATCCTTCATGAGGTATTTTGCTCACACCACTATT
                                                                                                                                                                                                                                                                                                                                                       1434
43
40
60
62
11
                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-613-486-15 (1-198) x US-10-138-842A-15 (1-1434)
           CURRENT APPLICATION NUMBER: US/10/138,842A
CURRENT FILING DATE: 2002-05-03
PRIOR PAPLICATION NUMBER: US 09/579,259
PRIOR PLING DATE: 2000-05-25
PRIOR PLING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/224,898
PRIOR FILING DATE: 1998-12-31
PRIOR FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: US 60/039,008
PRIOR FILING DATE: 1995-12-21
PRIOR FILING DATE: 1955-12-21
PRIMBER OF SEQ ID NOS: 67
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     904 Trigecgaraacggaagcreracagaraaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1354 ATGGCTTGCGCTATAGCGATTAAATCA
                                                                                                                                                                                                                                                           TYPE: DNA
, ORGANISM: Grapevine Leafroll Virus
US-10-138-842A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|||||:::
|1387 TTAAGGCGTAAAGGT 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuArgGinLeuGly 193
FILE REFERENCE: 07678/025006
                                                                                                                                                                                                                                                                                                                                                                     79.00
40.49%
20.98%
7.97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1327 CCGCCGCACGTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 IlePro----
                                                                                                                                                                                                                                                                                                                                                                       Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                             SEQ ID NO 15
LENGTH: 1434
                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \stackrel{>}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D,
```

```
------GGTCAAAAGAGAGTC 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValValThrGluGlyAspLeuLysLysValLeu------AspGlyCysAlaPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 LeuValileThrAspAlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGlu 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 ValGluLysMetLeuValGinLysGly------AlaProAsnGlu---GlyIleGlu 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 ValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysValGln 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ArgAlaAspSerAspValllePheSerAsnSerPheGlyGluArgAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                    .;
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1434
443
40
60
62
11
                                                                                                                                                                                                      Doyle
                                                                                         AFFLICANI LING KAI-Shu
IIILE OF INVENTION: GRAPEVINE LEAFROLL VIRUS
PROTEINS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-613-486-15 (1-198) x US-10-039-112-15 (1-1434)
                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      060 GACGGSTATAGGGTGGAGACCGAATTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/621
TELECOMFUNICATION INFORMATION:
TELEPHONE: (716) 263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            924 TIGCCGATAACGGAAGCICTACAGATAAAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/039,112
FILING DATE: 31-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DCS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
PAPPLICATION UNMBR: US 60009008
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: US-10-039-112-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Goldman, Michael L.
US-16-039-112-15

Sequence 15, Application US/10039112

Publication No. US2003C198942A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1434 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                 APPLICANT: Gonsalves, Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.931
79.00
40.49%
20.98%
7.97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COPOLOGY: linear
                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                            STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

us-09-613-486-15.rnpb

SEQUENCE DESCRIPTION: SEQ ID NO: 222: US-09-C70-927A-222	1) x US-09-070-927A-222 (1-1159' 12CCAGAGGACTCGAATGGTCAGTGGATATGGTGAAATTCAAGGAATGGTGCAGTGAATGGTGAAATTCAAGGAATGGTGAAAGCGTGAAGGAGGGTTATATCAGGAATGTTTATCAGTAATTAGGTGAAATTCAAGGAAGTGTTTAGCTTTTATCAGTAAGTTTAGCCACTTTATATTAGGTGAAATTGCCACTTTTATCAGGAAGTGTTTAGCCACTTTAGTGTTTAGCCACTTAGGAATTGCCACTTTTAGTGTTTAGCCACTTAGGAATGTTTAGTGTTTAGGTGAATTGCCACTTAGGTGAAAAGGATGATTAGCCACTTAGGTGAAAAGGATGATTAGCAGAATGCCAAAAAGGATGATTAGGTGAAAAGGATGATTAGGTGAAAAGGATGAT
Db 1102 TACTTAAGTATTCGGAAGTAAGGGAAGCTATTTAGGAGGGAAATACGGTGCGTCCCA 116: Cy 101 LeuThrArgPheThrAshiysLeuArgThrPheGlyArgThrPheThrGluAlaTyrVal 120 Db 1162ACAACTGTGCGATCCTTCAGAGTATTTGCTCACCACTATT 1209 Cy 121 AspPheCysIcalaTyrLysHightsLeuProGlnicuAshalaAlaGluicuI 140 Cy 121 AspPheCysIcalaTyrLysHightsLeuProGlnicuAshalaAlaGluicuI 140 Db 1210 ACTCTACTTATAGAGAAAATTCAGCCAGGGTGTACTGCCTAAGCTAAG	IlePro

Ŋ

us-09-613-486-15.rnpb

```
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
APPLICANT: Howard, Bussey
APPLICANT: Howard, Bussey
APPLICANT: Howard, Gene Disruption Methodologies for Drug Target Discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 TITCIGCGGGAIGAIGACACAGIGAAAGIAAGCCGGICCATTAAAGAATTAAGCAATAA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 TyrLeuAlaAspPhe-LeuGlyThrCysProLysLeuSerGluLeuGlnGlnSerAr 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 LeuargThrPheGlyArgThrPheThrGluAlaTyrValAspPheCysIleAlaTyrLys 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 HislysLeuProGinLeuAsnAlaAlaAlaGlu---LeuGlyIleProAlaGluAspSer 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----CAATCCAT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    00 CGGGATTCGATCGTCAACCATAACACGTCTCGTCTGGTCAGTGGTTCAACGTTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 ValGlnLysGlyAlaProAsnGluG;VIleGluVal-----ValPheGlyLeuLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 TyralaLeuAlaAlaArgThrThrSerProLysValGlnArgAlaAspSer---AspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 ATTGGTTTA--------ATTAAGTCTGTCGACAAATTTGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 IlePheSerAsnSerPheGlyGluArgAsnValValValThrGluGlyAspLeuLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTATCCGATAAACAAGTGAAAGAGCTTATTGCAAAAAGCCAGGAAGGCGACACAGAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGluValGluLysMetLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Valleu-----AspGlyCysAlaProbeuThrArg------PheThrAshlys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               665
33
67
11
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 ATCCGCAAAGCAAAGACGAACTGACGAAAACGCTG-----
                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-613-486-15 (1-198) x US-09-974-300-5760 (1-665)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 MetSerAspSerAsnLeuSerAsnLeuValIle----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glysMetPheAlaSerMetTyrAlaLeuLys 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496 GAAACGGTTTATGAAATGACGGCGATCCGA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454 GTATTTGCTGGAGATGCCAACCGGAGCTTGTCCT-
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: PastSEQ for Windows Version 4.0
SOFTWARE: 650
LENGTH: 665
TYPE: DN
ORGANISM: Bacillus clausi:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6808, Application US/10032585 Publication No. US20030180953A1 GENERAL INFORMATION:
                                                                                                                                                                                                      Ö
                                                                                                                                                                                                        ör
                                                                                                                                                              ) NAME/KEY: misc_feature

.0CATION: (1)...(665)

. THER INFORMATION: n = A,T,C

US-09-974-300-5760
                                                                                                                                                                                                                                                                                   0.451
77.50
40.84%
23.56%
7.82%
                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-032-585-6808
                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         신
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315091 GCTCTTCAGTCGCGTCTCGCGCCGGGTCACGTCTTTCTTCCCCCCTCTATGCGALCGCCTC 315150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314743 ---GGAACCGGCAAAAACTICTGGCACGGGGTATCATGAAGCTGCCAGACGTTCCGGC 314799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314800 ASCAAGCTCATCAGCTCAGAAGACGCAAGTGGGGAATCGCTTTTTGGCTTCGCCCCGAGC 314859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314860 GAGGGGGGGGAGGAGGTGCTTGGGCTACTCCAATACCATCCCAAAGCAACCCTGCTGATC 314919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314962 ATAGAAGTCATCGAGACAGGCGCTTATCGGCGCCTGGGCGACAAC-----GAGAGAGGG 315015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----- 315033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315034 Arcardechreaecedecaractrechaerraserreaecesscache---Arace 315090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValValValThrGlu---GlyAspieuLysiysValleuAspGlyCysAlaProieuThr 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 CysllehlaTyrLysHisLysLeuProGinLeuAsnAlahlaAlaGluLeuGlyIlePro 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----AlaAspPheleu 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 ArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPhe 122
                                                                                                                                                                                                                                                                                                                                                                                                                                             40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- AlaProAsr 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 ProLysValGinArgAlaAspSerAspValilePheSerAsnSerPheGlyGluArgAsn 83
                                                                                                                                                                                                                                                                                                                                                              1 MetGluLeuMetSerAspSerAsnLeuSerAsnLeuVallleThrAspAlaSerSerLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnGlyValAspLysLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 GluGiyileGluValValValPheGlyLeuLeuLeuTyrAlaLeuAlaAlaArgThrThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315151 GAAGATCTTCCACTCCTAGCTGAACACTTCCTACAAGCGCTCCGAAAG 315198
                                                                                                                                                                                                                                                                                                                                                                                                 314692 ATCGAAAAGCTTGCCGCTTCTAGTCTCCCGGTCATGATTACCGGACAAGCC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 GlyThrCysProlysLeuSerGlu----LeuGlnGlnSerArgLys 167
                                                                                                                                                                             536165
51
24
65
56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5760, Application US/39974306
Batent No. US20020146721A1
GENERAL INFORMATION.
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, 1b Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                        Conservative:
Xismatches:
Indels:
                                                                                                                                                                                                                                                                                                                      US-09-613-486-15 (1-198) x US-09-939-964-1 (1-536165)
                                                                                                                                                                                   Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315016 CGGTTCGAAGGCCGCCTG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: 60/279,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 AlaGluAspSerTyrLeuAla----
                                                                                                                                                                             1.17e+34
79.00
38.27%
26.02%
                    SOFTWARE: Patentin Ver. 2. SEQ ID NO 1 LENGTH: 536165 TYPE: DNA ORGANISM: Rhizobium
    NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-974-300-5760
                                                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                        US-09-939-964-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΩΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                             ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        င်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC
```

107

201

54

36

66

237

63

73

us-09-613-486-15.rnpb

ø

```
d
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               973 TATGACTCTAAAATAATACAGGTGAAAGAATTAACTAAAGAATTAGAAGATCACGCTAGA 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GAAATTGAAACAGATTTTCTT------CCAACG 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 AlaProLeuThrArgFheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAla 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 TyrValAspPheCysileAlaTyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGlu 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 LeuGlylleProAlaGluAspSerTyrLeuAlaAspPheLeuGlyThrCysProLys 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 LeuSerGlubeuGlnGlnSerArgLysMetPheAlaSerMetTyrAlaLeuLysThrGlu 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       874 AACGAGAACACCGATGACACCATTCATACCAGTAAAGTATAAAAGTTTTATTGAATATTGT 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           934 --------AATAATCTTCAAGCTAAAATCTTTACATGAAGAA 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 ThrSerProLysValGlnArgAlaAspSerAspVaillePheSerAspSerPheGlyGlu 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 ProAsnGluGlyIleGluValValPheGlyJeuLeuJeuJeuJeuAlaJaAlaArgThr 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 GlyValAspLysLysLeujeuSerAlaGluValGluLysMetLeuValGlnLysGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                              2 GlubeuMetSerAspSerAsrLeuSerAsnLeuVallleThrAspAlaSerSerLeuAsn 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------AATACCAAATTSGAACGACAAAATCATTACGTGACAAGGAAATT 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 GlyGlyValValAsnThrProValSerAsnLeuArgGlnLeuGlyArgArgGluVal 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 799 -----CAATTAGAAACTAAATATAATGATTTGTTTAAGGCATTG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 Arg-----AsnValValThrGluGlyAspLeuLysLysValLeuAspGlyCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2091
339
32
74
54
                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                             US-09-613-486-15 (1-198) x US-10-032-585-6808 (1-2091)
FILE REFERENCE: 10:82-005-999
CURRENT PEDIICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 6806
LENGTH: 2091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-10-156-761-4239
US-10-156-761-4239
Sequence 4239, Application US/10156761
Publication No. US/20030119018A1
GENERAL INFORMATION:
APPLICANT: OWNEA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (1209)..(1209)
OTHER INFORMATION: n=g, a, t cr
                                                                                                                                                                                                                                                                          3.3
77.00
35.68%
19.60%
7.77%
                                                                                                                         TYPE: DNA ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1033 -----
                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                          US-10-032-585-6808
                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      838
                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ДQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           검
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
772 AACGGCACCCCTGAACAGTCGGTTCAAGCCATTCGCGGACAGGGCGAGAAGCTGGCCGAC 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 TyrLysHisLysLeuProGlnLeuAsrAlaAlaAlaGluLeuGlyIle------ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 crescedesedesaceaegaceaegacergaarsaceaecaaegaceaecaecae---ereraesag 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GluAlaTyrValAspPheCysIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuAlaAlaArgThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 GlyCysAlaProLeuThrArgPheThrAsnLysLeu---ArgThrPheGlyArgThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----Argeadcreecenterces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 AsnSerPheGlyGluArgAsnValValValThrGluGlyAspLeuLysLysValLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Horne, Darci T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scheff, Uwe
APPLICANT: Gene Logue,
Inc.
ITILE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REPERENCE: 4921-5028-W0
CURRANT PELICATION NUMBER: US/09/880,107
CURRANT FILING DATE: 2001-66-1
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR APPLICATION NUMBER: US 60/237,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1068
124
123
238
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               982 Arccacreccedacreceacrecedes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 ------ProAlaGluAspSerTyrLeuAlaAsp 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-03-613-486-15 (1-198) x US-10-156-761-4239 (1-1068)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHORYIVIK
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PLILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 4239
LENGTH: 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 2228, Application US/09880107; Patent No. US20020142981A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.34
76.50
4C.71$
3C.09$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  946 GGCCGCCAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (1)..(1068)
US-10-156-761-4239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-39-880-107-2228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
```

115 89. 125 945

```
Query Match:
JB:
                                                                                                                                                                                                                                                                                                                                                                    22
                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                검
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6984 GCAGTGAGAAGGCGGCTGCTGTTCTTTCCTCCTCCAGCTGCCAGGACCTGGTGAGC 7043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7098 CAGGCAGCGGCCCCCTGAGACGT-----GGCGACTACAGAGCCTTTGGCCGCCTCATG 7151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 AspGlyCysAlaProLeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPhe 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 rLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSerArgly 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 SerAsmSerPheGlyGluArgAsmValValValThrGluGlyAspLeuLysLysValLeu 95
                                                                                                                                                                                                                                                                                                                                                                                                              56 AlaLeuAlaAlaArgThrThrSerProLysValGlnArgAlaAspSerAspValllePhe 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LeuProGlnLeu-AsnAlaAlaAlaGluLeuGlyIleProAlaGluAspSerTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7044 AAAGAGGCTTCCGGCGGCCCGGCACGTGGTG-----GGGGAGATTCGGCGCACGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 ThrGluAlaTyrValAspPheCyslleAlaTyrLysHisLys------
                                                                                                                         FEATURE:
CTHER INFORMATION: Genbank Accession No. US20020142981A1 576927
US-09-880-107-2228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7305 TGCTGTGCCTGGGGTTTATGGCAGCCGCATGACGGGCGGT 7344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 sMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGly 180
                                                                                                                                                                                                                                                                                                                                                                        US-09-613-486-15 (1-198) x US-09-880-107-2228 (1-8095)
                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CMURA, SATOSHI
APPLICANT: CMURA, SATOSHI
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIVUXI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-26
CURRENT APPLICATION NUMBER: US/13/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR PLILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                             33.7
76.50
38.06
23.88
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
                       SOFTWARE: Patentin Ver.
SEQ ID NO 2228
LENGTH: 8095
                                                                                     TYPE: DNA CRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 9025608
                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-156-761-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130
                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CP
```

```
NESUGE 12

ORGENOTE 12 SEQUENCE 2004/04 SPRICATION US/09864761

SEQUENCE 2004/04 SPRICATION US/09864761

SEQUENCE 2004/04901 SPRICATION US/09864761

SEQUENCE 2004/049763A1

SEQUENCE 2004/049763A1

SEQUENCE 2004/04/05 SINGLE EXON NUCLEIC ACID PROBES USFUL FCR APPLICANT: BANK, David R. APPLICANT: BANK, David R. APPLICANT: Chen, Wensheng

ITTLE OF INVENTION: HUMAN GENOME DERIVED SINGLE EXON NUCLEIC ACID PROBES USFUL CANT. Chen, Wensheng

ITTLE OF INVENTION: GENE EXPRESSION NALYSIS BY MICROARRAY

FILE REFERENCE: ACOUGLEA'-1

CURRENT PERING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRICR FILING DATE: 2000-05-26

PRICR FILING DATE: 2000-05-26

PRICR FILING DATE: 2000-09-27

PRIOR PAPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2001-09-27

PRIOR PAPLICATION NUMBER: PCT/US01/0066

PRIOR APPLICATION NUMBER: PCT/US01/0066

PRIOR APPLICATION NUMBER: PCT/US01/0066

PRIOR PRILNG DATE: 2001-01-30

PRIOR PLILNG DATE: 2001-01-30

PRIOR PRILNG DATE: 2001-01-30

PRIOR PRILNG DATE: 2001-01-30

PRIOR PRILNG DATE: 2001-01-30

PRIOR PRILNG DATE: 2001-01-30

PRIOR PLILNG DATE: 2001-01-30

PRIOR PRILNG DATE: 2001-01-30

PRIOR PLILNG DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5216916 AACGGCACCCCTGAACAGTCGGTTCAAGCCATTCGCGGACAGGCCGAGAAAGCTGGCCGAC 5216975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5216859 CTGGCGGGGGCCAGGCCAGGCCTGGGTGACCACCGGCGACCGGGG---CTGTACGAG 5216915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5217036 ACCCGGACCGCGGTCGCCCGCTGGAGTCCCTCGACGCGTTCGTCGACTTC-----GCG 5217089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 GlyCysAlaProLeuThrArgPheThrAsnLysLeu---ArgThrPheGlyArgThrPhe ils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuAlaAlaArgThrThrSerProLysValGlnArgAlaAspSerAspValIlePheSer 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AssSerPheGlyGluArgAsnValValValThrGluGlyAspLeuLysLysUalLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 TyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIle-----
                                                                                                                                                                                       9025638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5217126 ATCCACTGGCCCATCCCCGACTCGGACTTCGCCGCGGGAC 5217164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ProalaGluAspSerTyrLeuAlaAlaAsp 151
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-613-486-15 (1-198) x US-10-156-761-1 (1-9025608)
                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                   other or unknown
                                                                   ຫ
                                                                                                                                                                                       1.84e+06
                                                                   ο
                                                                                                                                                                                                                 76.50
40.71¥
30.09$
7.72$
                                                                   Ĺį
NAME/KEY: misc feature ; LCCATION: (4187715) ; OTHER INFORMATION: a, tUS-10-156-761-:
                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77
```

```
Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynuciectides and Polypeptides
NUMBER OF SQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
CCUNTRY: USA
                                              ---LeuGlyThrCysProLysLeuSerGluLeuGlaGlaSerArg 166
                                                                                             167 LysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrProVal i86
                                                                                                                                      ----cccacarrcccracaacraccrccrraccrcr 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --SerAlaGluValGlu 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 CPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 AlaSerSerLeuAsnGlyValAspLysLysLeuLeu----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-613-486-15 (1-198) x US-09-070-927A-238 (1-29729)
                                                                                                                                                                                       187 SerAsnLeuArgGinLeuGlyArgArgGluValMet 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
                                                                                                                                                                                                                     126 TCCTGGCTTTCACAACTGCGCCTCCTGAAACTGATG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/370,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <UNKnOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/C46,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/C44,031
FILING DATE: 1997-05-36
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATICN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPCLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
                                                                                                                                                                                                                                                                                                                         Sequence 238, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ 10 NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 29729 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.50
35.41%
21.53%
7.62%
                                                                                                                                         174 AAACCCTTCCTTGAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                   US-09-070-927A-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-070-927A-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
  153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
                                                                                                                               a
                                                                                                                                                                                                                                 Cp
                                       g
                                                                                        ò
                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||||::::::||
| TCTTTCCCGCAGCACAAATGGGTGGGGGCCCACTGTTAATTCTCTAAATTCCCCACCGGG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            579 detalactradecercegraceaecraaceaarrerserrragierereteiderdifetae 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          489 TCCTCAAACTITCTAGGACAITCCATCTIATTTACATCCTAITTCTTAAAGAAAGTAGAA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AspGlyCysAlaProLeuThrArgPheThrAsnLysLeuArgThrPheGly 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 ArgThrPheThrGluAlaTyrValAspPheCysIleAlaTyrLysHisLysLeuProGln 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------GACTGCCACCAAACCTACAGACCAACGCTCATCCACAACCTCTC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 CATAGGATCCTCTTTCTCTCCCACCTCCTTGCTTTCTGCATCTTTAACACCTACTTC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 AlaLeuAlaAlaArgThrThrSerProLysValGlnArgAlaAspSerAspValllePhe 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerAsmSerPheGlyGluArgAsnValValValThrGluGlyAspLeuLysLysValLeu 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -------GluValValPheGlyLeuLeuTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N: EXPRESSED IN HERRY, SIGNAL = 2.5

N: EXPRESSED IN HERRY, SIGNAL = 2.4

N: EXPRESSED IN BRAIN, SIGNAL = 2.4

N: EXPRESSED IN BRAIN, SIGNAL = 2.4

N: EXPRESSED IN BCMS MARROW, SIGNAL = 2.2

N: EXPRESSED IN HEAL, SIGNAL = 3

N: EXPRESSED IN HEAL, SIGNAL = 2.9

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
              PRIOR APPLICATION NUMBER: PCT/JSC1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PAPPLICATION NUMBER: PCT/JSC1/00663
PRIOR APPLICATION NUMBER: PCT/USC1/00662
PRIOR APPLICATION NUMBER: PCT/USC1/C061
PRIOR APPLICATION NUMBER: PCT/USC1/C061
PRIOR PILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2000-09-21
PRIOR PLILING DATE: 2000-09-21
PRIOR PLILING DATE: 2000-09-21
PRIOR PLILING DATE: 2000-09-21
PRIOR PLILING DATE: 2001-01-29
NUMBER OF SEQ 1D NOS: 49117
SEC ID NO 8204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 LeuAsnAlaAlaGluLeuGlyIleProAlaGluAsp----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SerTyrLeuAlaAlaAspPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-613-486-15 (1-198) x US-09-864-761-8204 (1-600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  519 ATGGTGGCAGTTTCCTCAATTTCTCCA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 ProAsnGluGlyIle-----
2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.631
76.00
34.90%
22.92%
7.67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION: EINFORMATION: EINFORMATION: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMAT
CTHER INFORMAT
US-09-864-761-8204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
```

d

ð S C ò a ઠે 30 ò g

ઠે

ద ò

ò

σ

```
64953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65130
                                                                                                                                                                                                                                                        64843 AAGATGACTCTGTGGGATGCCCCCACTCAT-----GACGGTTGTGCTCCCATA 64893
                                                                                                                                                                                                                                                                                                                                                                                                                             64954 AAATGTGAAGCCCAAAGTTACACTGCCATTAAACTAATAAACGGCAATGAATACCAATTC 65013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Munger, William E.
APPLICANT: Munger, William E.
APPLICANT: Kulkarni, Prakash
APPLICANT: Kulkarni, Prakash
APPLICANT: Kotzenberg, Robert H.
APPLICANT: Waga, Iwao
APPLICANT: Waga, Iwao
APPLICANT: Wamanoto, Jun
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatio
TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
CURRENT APPLICATION NUMBER: US/09/873,319A
CURRENT FILING DATE: 2001-06-05
EARLIER APPLICATION NUMBER: US 60/223,323
EARLIER FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
                                                                                                                                                                                                                                                                                                                                                                                        128
                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 LysleuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAspSerTyrLeu 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 AlaAlaAspFheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnGsrArgLysMet 168
                                                                       65
                                                                                                                                                                                                                       ArgAsnValValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaProLeu
                                                                                           GTACAAGATACACCAGGAAAAGTAGTTGGGCCAATAAGATTCACCAATATTACTGGGGAG
                                                                                                                                                                                                                                                                                                        102 ThrArgFheThrAsmLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAsp
                                                                                                                                                                                                                                                                                                                                                                                        --TyrLysHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65071 GTIGCICAAATACAATATATATGTTCCTGATGCCCTGGCATTCCAGAACCTAGCAACATA
                                                                       -ProLys
                                                                                                                                              ValginArgAlaAspSerAspValIle-----PheSerAsnSerPheGlyGlu
                                                                                                                                                                                                                                                                                                                                            64894 ACCCACTACATGAAAAACGGGAAACCAGCAGACTTGCCTGGGCACTAATTGAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65014 CGTGTTTCTGCAGTTAACAAGTTGGT---GTTGGCAGGCCACTTGATTCTGATCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---- LysThrGluGlyGlyValValAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65131 ACAGGCAACAGCATTACCCTGACATGGGCAAGGCCAGAATCAGATGGTGGC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Genbank Accession No. US20030134324A1 X90568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AGTGAAATTCAACAGTATATCCTTGAAAGAAGAA 65217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 ThrProValSerAsnieuArgGln-----LeuGlyArgArgGlu 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339
727
67
78
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                           US-09-613-486-15 (1-198) x US-09-759-508B-1 (1-81940)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                54 LeuTyrAlaLeuAlaAlaArgThrThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 724, Application US/09873319A Publication No. US20030134324A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        122 PheCysileAla------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PhealaSerMetTyrAlaLeu--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.22e+03
75.00
37.71%
22.29%
7.57%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patent
SEQ ID NO 724
LENGTH: 81940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-873-319-724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-873-319-724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                     64783
                                                                                                                                                                                                                             82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65182
                                                                                                  30
                                                                                                                                              ò
                                                                                                                                                                           20
                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                              23
                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                        CD
                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                         Ω.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      े
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GAA 13730
13176 GCAGGCGGTATGCGGGGGGNTTGAGTTTACTTTTCTCTCAAGCAACAGAAGTSATT 13235
                                                                                                                                                                                                                                       13344 ATTGTGAGTCCAAGCTTCCATGAAGAAACCGCTAAAATTTGCAATTTATATCAAGTTCCT 13403
                                                                                                                                                                                                                                                                                                                         ----GCAGGGGCTGAATAT 13343
                                                                                                                                                                                                                                                                                                                                                                                                        13514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13515 TTTAAAGCGCCATTGCCTCAGTTAAATATTATGCCAACGGGTGGTGTCAGTTTGGAAAAT 13574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149
                                                                                                                                                                                                                                                                                                                                                                                                                                            126 TyriysHisLysieuProGlnieuAsnAlaAlaAlaGluieuGlyileProAlaGluAsp 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 PheAlaSerMetTyrAlaLeulysThrGluGlyGlyValValAsnThrProValSerAsn 188
                                         34 LysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPheGlyLeuLeu 53
                                                                                                                                                                                                                                                                                                                                                                 .3464 ATTATTAAACTATTTCCGGGAAGTGTTTATGGACCGAGTGTTATTCA------GCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13575 ATGGCCGAGTGGTTCGCTGCAGGTGTGACGGCCGTCGGTGTTGGTGGCAATCTGTTAGCG
                                                                                                                         LeuTyrAlaLeuAlaAlaArgThrThrSerProLysValGlrArgAlaAspSerAspVal
                                                                                                                                                                                                                                                                                 94 ValleuAspGlyCysAlaProLeuThrArgPheThrAsnLysLeuArgThrPhe----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 -----SerTyrLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 AlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGinSer---ArgLysMet
                                                                               13236 CAGGAATTAGTTGCGTTATACCAAGAGAATCCTGACGTAGTCATTGGTGCGGGGACAGTT
                                                                                                                                                                                                      ilePheSerAsnSerPheGlyGluArgAsnValValValThrGluGlyAspleuLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/39759508E
Sublication No. U320620182593A1
GENERAL INFORMATION:
APPLICANT: Fishman, Mark C.
TILLE OF INVENTION: Methods for Diagnosing and Treating Heart Disease
FILE REFERENCE: 00786/381002
CURRENT APPLICATION NUMBER: US/03/759,508B
CURRENT FILING DATE: 2031-01-12
PRICR APPLICATION NUMBER: US 60/175,787
PRICR FILING DATE: 2000-01-12
NUMBER OF SEC ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81940
39
27
67
42
                                                                                                                                                              13296 TTGGATGCTACGACTGCTCGTTTAGCTATTGTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13695 TTCCAAGCAATCAAAGGGGTGTAGGCACATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13731 AGTCGTAACATTGGGAGAAATCATGTT 13757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 LeuArgGlnLeuGlyArgArgGluVal 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.22e+03
75.00
37.71
22.29%
7.57%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin version 3.1 SEQ ID NO 1 LENGTH: 81940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (80910)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (133)...(
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-759-508B-1
                                                                                                                         54
                                                                                                                                                                                                    74
                                                                                                                                                                                                                                                                                                                                                                 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                          S
                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                                                                                                                                                                                                                                                                                    υp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                         ò
                                                                               ΩĎ
                                                                                                                       ठे
                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  긤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ठे
```

```
64894 ACCCACTACATCATTGAAAAACGGGAAACCAGCAGACTTGCCTGGGCACTAATTGAGGAT 64953
                                                                                                                                                                                                                                                                                                                                                                                                    ----- 65181
                                                                                                                                         129 LysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAspSerTyrLeu 148
                                                                                                                                                                                                                                                                                                                        149 AlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSerArgLysWet 168
                                                                                                                                                                                                                                                                                                                                                                           169 PhehlaSerMctTyrAlabeu-------LysThrGluGlyGlyValValAsn 183
                                                                                                                      82 ArgAsnValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaProLeu 161
                                                                                                                                                                          102 ThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAsp 121
                                                                                                                                                                                                                          122 PheCysleAla----TyrLysHis 128
                         ----Prolys 65
                                                                       ----PreSerAsnSerPheGlyGlu 81
                                                                                                                                                                                                                                                                                                                                                                                              184 ThrProValSerAssicuArgGin-----LeuGlyArgArgGlu 196
US-09-613-486-15 (1-198) x US-09-873-319-724 (1-81943)
                       54 LeuTyrAlaLeuAlaAlaArgThrThrSer---
                                                                       66 ValGlnArgAlaAspSerAspValIle----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: November 8, 2003, 03:17:34 Job time : 2632 secs
                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                          8 6 8
                                                                                                                                                                                                                                           qc
                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                               QC
                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                        ò
                                          d
                                                                       ò
                                                                                           g
                                                                                                                 à
                                                                                                                                                                                                                    ò
```

```
coat protein - sug-
coat protein - sug-
capid protein - sug-
day protein protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
probable GDS.-moti
probable GDS.-moti
hypothetical protein
hypothetical hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  flagellin - Thermo
penicillin-binding
formate-tetrahydro
                                                                                                                                                        November 7, 2303, 14:47:08 ; Search time 21 Seconds (without alignments) 906.733 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                        US-09-613-496-15
991
1 MELMSDSNLSNLVITDASSL.......GGVVNTPVSNLRQLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283308 segs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                            - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             $22900
$22800
$22801
$22801
$22809
$24289
$24289
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
$2801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B97363
D70176
H72217
E82815
                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             %
Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317
714
714
387
873
555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR 76: *

1: pir1: *

2: pir2: *

3: pir3: *

4: pir4: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing:
                                                                                                                                                                                                                                                                        Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                         OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
```

hypothetical prote cytochrome 9450 Cy orotate phosphorib probable two-compo hypothetical prote probable sodium/hy hypothetical prote probable sodium/hy hypothetical prote hypothetical prote (S)-2-hydroxy-acid cyclin A-type (alo vacuolar protein s translation initia methyltransferases	AJIGNMENTS	sugar beet yellows virus ar beet yellows virus, SBY 1.995 steequence_revision O6-Jan.1995 #text_change 11-Jan.2000 1.9900, 534200 1.9006. 534200 1.9006. 534200 1.9006. 534200 1.9006 1.9006. 534202 2.9006. 50. 60. 50. 60. 50. 60. 50. 60. 50. 60. 50. 60. 50. 50. 60. 50. 50. 60. 50. 50. 60. 50.	otein - sugar beet yellows virus es: sugar beet yellows virus, SBYV 07-May-1953 #sequence_revision 07-May-1993 #text_change 11-Jan-2000
A13234 A13234 B43234 B43236 C83151 C731615 C731615 C731616 C7316 C7316 C7316 C7316	ALIG	theet yellows virus, sBYV #sequence_revision 06-Jan. # \$34206 # \$34206 # Badauce_revision 06-Jan. # \$34206 # Baley, J.; Hull, R. # Bull Library, August 19: # \$27898 # # # # # # # # # # # # # # # # # # #	yellows virus ows virus, SBY ince_revision 0
000000000000000		10 10 10 10 10 10 10 10 10 10 10 10 10 1	10.5
320 208 208 308 308 208 208 208 208 208 208 208 208 208 2		sugar beet yellows leet yellows virul 1995 #sequence_revi 7900; \$34206 in Moseley, J.; Hull willoutide sequence 7900 minary 1000	beet yel yellows
00000000000000000000000000000000000000		- sugar be gar best yr n-1995 ets yr n-1995	sugar b r beet 1993 #s
c. c		Accession: 25 Accession: 25 Accession: 32 Access	protein - cies: suga e: 07-May-
ij m m m m m m m m d d d d d d d d d d d		RESULT 1 S27900 Coat protein - sugar beet yellows virus, C;bate: 06-Jan-1995 #sequence_revision C;Accession: S27900; S34206 R;Brunstedt, J; Moseley, J; Hull, R Submitted to the EMBL Data Library, A;Description: Nucleotide sequence of A;Accession: S27900 A;Status: preliminary A;Accession: S27900 A;Status: preliminary A;Accession: S27900 A;Actus: preliminary A;Accession: S27900 A;Actus: preliminary A;Accession: S34206 A;Accession: S34206 A;Accession: S34206 A;Accession: S34206 A;Accession: S34206 A;Accession: S34206 A;Catus: preliminary A;Residues: 1-204 AGR> A;Accession: S34206 A;Catus: preliminary A;Residues: 1-204 AGR> A;Cassreferences: EMBL*X3475; NID: C;Superfamily: SBV probable coat procuery Natch A;Cassreferences: EMBL*X3475; NID: C;Superfamily: SBV probable coat procuery Natch A;Cassreferences: EMBL*X3475; NID: C;Superfamily: SBV probable coat procuery Natch A;Cassreferences: EMBL*X3475; NID: C;Superfamily: SBV probable coat procuery Natch A;Cassreferences: EMBL*X3475; NID: C;Superfamily: SBV probable coat procuery Natch A;Cassreferences: EMBL*X3475; NID: C;Superfamily: SBV probable coat procuery Natch A;Cassreferences: EMBL*X3475; NID: C;Superfamily: SBV probable coat procuery Natch A;Cassreferences: EMBL*X3475; NID: C;Superfamily: SBV probable coat procuery Natch Batches 71; Conservative 31; C;	

```
200 SSVDGKIV----SLFDLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 LKTEGGWWNTPVSNLRQLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.0%
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
C49804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECX.
                  RiAgranovsky, A.A.; Boyko, V.P.; Karasev, A.V.; Lunina, N.A.; Koonin, E.V.; Dolja, V.V. J. Gen. Virol. 72, 15-23, 1991.
A.Title: Nucleotide sequence of the 3'-terminal half of beet yellows closterovirus RNA systerence number: S28710; MUID:91116305; PMID:1990061
A.Reference number: S28710; MUID:91116305; PMID:1990061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   capsid protein p25 - citrus tristeza closterovirus CTV
C;Species: citrus tristeza ciosterovirus CTV
C;Decies: ll-Cot-1994 #sequence_revision 25-Apr-1997 #text_change ll-Can-2000
C;Accession: D49804
R;Pappu, H.R.; Karasev, A.V.; Anderson, E.J.; Pappu, S.S.; Hilf, M.E.; Febres, V.J.; S.M.; Dawson, W.O.; Lee, R.F.; Niblett, C.L.
S.M.; Dawson, W.O.; Lee, R.F.; Niblett, C.L.
A;Title: Nucleotide sequence and organization of eight 3' open reading frames of the A;Reference number: A49804; MUID:94160579; PMID:8116253
                                                                                                                                                                                                                                                                                                                                                                                                                     67 QRADSDVIFSNSF-GERNVVVTEGDLKKVLDGCAPLIRFTNKLRTFGRIFTEAYVDFCIA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVQPISTFIKASFGGGKELYLTHGELN8FJGSQKLLEGKPNKLRCFCRTFQKDYISLRKE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 YKHKIPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGGVVNTP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 APLTRFINKLRTFGRTFTEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 -----TNALRVWGRTNDALYLAFC-RQNRNLSYGGRPLDAGIPAGYHYLCADFL-TGAG 184
                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 ARTIS------PKVQRAD---SDVIF-SNSFGERNVVVTEGDLKKVLDGC 98
                                                                                                                                                                                                                                                                                                                                7 SNLSNLVITDASSINGVDKKLLSAEVERMLVQKGAPNEGIEVVFGLILYALAARTTSPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PNEGIEVVFGLLLYALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 SSVNLHIDPTLITMNDVRQLSTQQNAALNRDLFLTLKGKHPNLPDKDKDFHIAVMLYRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 VKSSŠLQSDDDATGITYTREGVEVDLSDKLWTDVVFNSKGIĞNR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Note: sequence extracted from NCBI backbone (NCBIN:144092, NCBIP:144102)
A.Note: severe quick decline isolate 136
C.Superfamily: SBYV probable coat protein
                                                                                                                             A;Molecule type: DNA
A;Residues: 1-204 <AGR>
A;Cross-references: EMBL:X53462; NID:g58878; PIDN:CAA37554.1; PID:g58883
C;Superfamily: SBYV probable coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 223;
                                                                                                                                                                                                                                              Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Indels
                                                                                                                                                                                                                                                                                          87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSELQQSRKMFASMYALKTEGGVVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                          Query Match 28.9%; Score 286; DB 2; Best Local Similarity 37.6%; Pred. No. 3e-19; Matches 71; Conservative 29; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.6%; Score 125; DB 2;
25.9%; Pred. No. 0.00036;
tive 33; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 SSLN-GVDKKLLSA-EVEKMLVQKGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: D49804
A,Status: preliminary
A,Molecule type: genomic RNA
A,Residues: 1-223 APAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTSLKOLGR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 56; Conserva
C, Accession: S28715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
249804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ω̈́,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                  ે
                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
C. Accession: 534205
R. Agramovsky, A.A.; Koonin, E.Y.; Boyko, V.P.; Maiss, E.; Lunina, N.A.; Atabekov, J.G.
R. Agramovsky, A.A.; Koonin, E.Y.; Boyko, V.P.; Maiss, E.; Lunina, N.A.; Atabekov, J.G.
Submitted to the EMBL Data Library, June 1933
A. Description: Complete nucleotide sequence of the Ukrainian isolate of Beat yellows vi
A. Reference number: 534205
A. Accession: 534205
A. Accession: 534205
A. Retainiary
A. Molecule type: genomic RNA
A. Residues: 1-216 AGR>
A. Residues: 1-216 AGR>
A. Cross_references: EMBL:X73475; NID:g313639; PIDN:CAAS1860.1; PID:g313633
                                                                                                                                                                                                                                                 of beet yellows vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DECIAYKHKLPQLN---AAAELGIPAEDSYLAADFL---GTC----PKLSELÇQSRKMFA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 KVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTBAYVDFCI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 AYKHKLPQL---NAAAELGIPAEDSYLAADFL---GTC----PKLSELQQSRKMFASMYA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
Expectational protein 2 - sugar beet yellows virus
Cispectes: sugar beet yellows virus
Cispectes: sugar beet yellows virus, SBYV
Cibate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
Ciscession: S27899
RiBrunstedt, J.; Moseley, J.; Hull, R.
Submitted to the EMBL Data Library, August 1991
A.Description: Nucleotide sequence of CDNA encoding the coat protein of beet A;Reference number: S27899
A.Stetus: 227899
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-216 ABRU-
A.Residues: 1-216 ABRU-
A.Residues: RBBL:M59452; NID:G323237; PIDN:AAA72954.1; PID:G323239
Cisuperfamily: SBYV probable coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coat protein homolog - sugar beet yellows virus
Clopedies: sugar beet yellows virus, SBYV
Clobace: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 10-Dec-1999
Clobacession: S342C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TISPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLIRFTNKLRTFGRIFTEAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 ---IVIARSLPKININRTIGKRGIPSGYEFLGADFLTATSVCLNDHEKAIVLQASRAAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 KVNYVGA---YEYTIGGKKFLVKDAWVFPLIKECMKKFNKPNPVRTFCATFEDAY----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 SDSNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 SEVNPNKLNRKETDELLGVIRERFKSELV-----ITDEDFVKHLAFALIRAANITTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.5%; Score 104, DB 2; Length 216; Best Local Similarity 28.5%; Pred. No. 0.632; Matches 41; Conservative 19; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.1%; Score 100.5; DB 2; 25.0%; Pred. No. 0.067; tive 27; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 SMYALKTEGGUVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 RAVSSSVDGKIV----SLFDLGR 214
```

```
A;Residues: 1-1692 <YOU'>
A;Residues: 1-1692 <YOU'>
A;Cross-references: GB:MZ6699; NID:g173338; PIDN:AAA35284.1; PID:g173339
A;Cross-references: GB:MZ6699; NID:g173338; PIDN:AAA35284.1; PID:g173339
R;Yamawaki-Kataoka, Y.; Tamacki, T.; Choe, H.R.; Tanaka, H.; Kataoka, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 56,93-5667, 1989
A;Title: Adenylare cyclases in yeast: a comparison of the genes from Schizosaccharomyce A;Reference number: A33539; MUID:89345533; PMID:2668944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Superfamily: yeast adenylate cyclase, leucine-rich alpha-2-glycoprotein repeat homolo C:Keywords: phosphorus-oxygen lyase F;1328-1413/Domain: yeast adenylate cyclase catalytic domain homology <YACC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 20nl. A.; Akhuthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Stex, E.W. A,fittle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1692 <LYN>
A;Cross-references: EMBL:AL023859; PIDN:CAA19571.1; GSPDB:GN00067; SPDB:SPRC19C7.
A;Experimental source: strain 972h-; cosmid c19C7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 TEGDLKKVLDGCAPLTRFINKLRT----FGRTFTEAYVDFCIAYKHKLPQLNAAAELGIF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 TIMDI -----GADVLRKFSEKKITANLDISRSNLEVIPVKIYPYAHELISLNVSHNLSLD 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 LLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKVQRADSDVIFSNSFGERNVVV 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-450 monooxygenase virHl [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                adenylate cyclase (EC 4.6.1.1) - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Date: 23-Mar-1990 #seguence revision 23-Mar-1990 #text_change 31-Mar-2000 C; Accession, A33989, A33519, T3989 A37519, T3989, A3; T3989, A3; T3989, A3; T3989, A3; T3040, D.; Riggs, M.; Field, C.; Vojtek, A.; Broek, D.; Wigler, M. Proc. Natl. Acad. Sci. U.S. A. 86, 7399-793, 1389 A; Title: The adenylyl cyclase gene from Schizosaccharomyces pombe. A; Reference number: A3988; MUID:90046723; PMID:2682634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Agrobacterium tumefaciens
C;Date: i1-Jan-2002 #sequence_revision 11-Jan-2002 #text_change :8-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Residues: 1-1692 (*XAM)
A, Cross-references: GB:M24942; NID:g173378; PIDN:AAA35301.1; PID:g173379
A, Cross-references: GB:M24942; NID:g173378; PIDN:AAA35301.1; PID:g173379
A, Note: the authors translated the codon TGC for residue 626 as Ser, and 68. Lyne M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C. submitted to the EMBL Data Library, June 1998
A, Accession: T19809
A, Accession: T19809
A, Status: preliminary; translated from GB/EMBL/DDBC
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 AEDSYLAADFLGTCPKLSELQQSRKMFASMYAJKTEGGVVNTPVSNLRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LPLDFYERCVKLKRIDISNN-----LRSFRG---KPITALRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
9.1%; Score 92; DB 2; Length 1692;
Best Local Similarity 24.7%; Pred. No. 5.9;
Matches 42; Conservative 26; Mismatches 68; Indels
SSVDGKIV----SLFDLGR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: SPBC19C7.03
A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: AD3246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: A33539
200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                C.Species: citrus tristeza closterovicus CTV
C.Date: il-Oct-1994 #sequence_revision 25-Apr-1997 #text_change 11-Jan-2000
C.Date: il-Oct-1994 #sequence_revision 25-Apr-1997 #text_change 11-Jan-2000
R.Pappu, H.R.; Karasev, A.V.; Anderson, E.J.; Pappu, S.S.; Hilf, M.E.; Febres, V.C.; Eck
S.M.; Dawson, W.O.; Lee, R.F.; Niblett, C.L.
A.Ntology 199, 33-46, 1994
A.Title: Nucleotide sequence and organization of eight 3' open reading frames of the cit
                                                                                                                                                                                                                                                                                                                                                     A,Accession: C49804
A,Status: preliminary
A,Molecule type: genomic RNA
A,Molecule type: genomic RNA
A,Residues: 1.240 e PAP>
A,Cross-references: GB:U16304; GB:U22547; GB:L20760; N:D:g806738; PIDN:AAC59629.1; PID:g
A,Note: sequence extracted from NCBI backbone (NCBIN:144092, NCBIP:144099)
A,Note: severe quick deciline isolate T36
C,Superfamily: SBYV probable coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Accession: $28714

R;Agranovsky, A.A.; Boyko, V.P.; Karasev, A.V.; Lunina, N.A.; Koonin, E.V.; Dolja, V.V.
J, Gen. Vizol. 72, 15-23, 199

A;Tile: Nucleotide sequence of the 3'-terminal half of beet yellows closterovirus RNA A;Tile: Nucleotide sequence of the 3'-terminal half of beet yellows closterovirus RNA A;Reference number: $28710; MUID:91116305; PMID:1990061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٠.
سا
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKFTGEHLKYVXVTMDTFLLENYKTKTBDLLVHLTMIÇK--------RLYTI--- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTSPKVQRADSDVIFSNSFGERNVVVTEGDLK-KVLDGCA---PLTRFT----NKLRTF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 ACTPEELHI--CMARLRPDLYENK----RTTRAGTPHLKGYLSADFLSGSLPGYSEHER 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 KVQRAJSJVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 KVNYVGA---YEYIIGGKKFLVKDAWVFPLIKECMKKFNKPNPVRTFCAIFEJAY----I 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 AYKHKLPQL---NAAAELGIPAEDSYLAADFL---GTC----PKLSELQCSRKMFASMYA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 VIARSIPKLFLNRTIGKRGIPSGYEFLGADFLTATSVCLNDHEKAIVLQASRAAIDRAVS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 GRTFFTEAYUDFCIA-----YKHKLPQLNAAAELGIPAEJSYLAADFL-GTCPKLSE--- 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 SDSNLSNLVITTDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 SEVNPNKLNRKETDELLGVIRERFKSELV-----ITDEDFVKHLAFALIRAANITISV 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              $28714
hypothetical protein 5 - sugar beet yellows virus
C;Species: sugar beet yellows virus, SBYV
C;Species: 07-May-1993 #sequence_revision 07-May-1993 #text_change 10-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ELMSDSNLSNLVIT-DASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 STSTKTKFRDKGCI-----SYVQGGLRYKLJDKVVFPFIISKFTDRETPNALRKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: DNA
A,Residues: 1-216 <AGR>
A,Cross-references: EMBL:X53462; NID:g58878; PIDN:CAA37553.1; PID:g58882
C,Superfamily: SBYV probable coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.1%; Score 100.5; DB 2; Length 240; Best Local Similarity 26.4%; Pred. No. 0.077; Matches 57; Conservative 28; Mismatches 70; Indels 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.0%; Score 99.5; DB 2; Length 216; Best Local Similarity 25.0%; Pred. No. 0.083; Matches 50; Conservative 27; Mismatches 94; Indels 2
capsid protein homolog p27 - citrus tristeza closterovirus CTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---LOQSRKMFASMYALKTEGGVVNTPVSNLRCLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 LKTEGGVVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S28714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ω̈́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

GCC for residu

C;Genetics:

```
PB94722
probable GDSL-motif lipase/hydrolase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: D2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: B84722
R;Lin, X: Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
X.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Recence number: A84420; MJD:20083487; PMID:10617197
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Cross-references: GB:AEC02093; NID:q4582450; PIDN:AAD24834.1; GSPDB:GN00139
C;Gene: At231550
A;Gene: At231550
A;Map position: 2
C;Superfamily: myrosinase-associated protein MyAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       psignostic dispase/hydrolase [imported] - Arabidopsis thaliana cyspatias arabidopsis thaliana (mouse-ear cress) cyspecies Arabidopsis thaliana (mouse-ear cress) cyspecies arabidopsis thaliana (mouse-ear cress) cybrus a84722 for a84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                      77 NSFGE--RNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIAYK-HKLPQL 133
                                                                                                                                                                                                            289 IRFGSVLENVVVDED-----ATREANYDDSFYTENTRA-----AYPIHMINNI 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 LSDQDILTGVCFASAGIVGDXKAMEIINNAFVVVSAGPND----FILNYYDIPSRRLEY 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 KVQRADSDVIFSN-----SFGERNVV/TEGDLKKVLDGCAPLTRFTNKLRTFGRTF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 PFISGYODFILKRLENFVRELYSLGVRNVLV--GGLPPM--GCLPI-HMTAKFRNIFRFC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 TEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYAL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 JEHHNKDSVLYNEKLQKLLPQIEASLPG-SKFLYADVYN--PMMEMIQNPSK-----YGF 266
234 LSGTGKTTLSADADRKLIGDDEHGWSDTGVFNIEG-GCYAKCIHLSEEK----EPQIFNA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:AE002093; NID:94582449; PIDN:AAD24833.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 ITDASSLNGV-----DXKLLSAEVERMLVQKGAPNEGIEVVFGLLYALAARTTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                         331 VIPSMAGHPSAIVFLADAFGVLPPISKLIKEQVMYHFLSGYTSKLAGTERGVTS 385
                                                                                                                                                                                                                                                                                                        134 NAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKM--FASMYALK---TEGGVVN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.7%; Score 86.5; DE 25.8%; Pred. No. 2.3; tive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 25.8
tes 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-TEGGVVNT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 KETKRGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-360 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: At2g31540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                 8
                                                                                                                                                                                       C,C
                                                                                                                                                                                                                                                                                                   ठ
                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphoenolpyruvate carboxykinase pckA - Bacillus subtilis
CiSpecies: Bacillus subtilis
CiSpecies: Bacillus subtilis
CiOate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
CiOate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
CiStocession: F65673
Ekkunst, F.; Cgasawara, N.; Moszer, I.; Albertin.; A.M.; Alloni, G.; Azevedo, V.; Berter
Ci, Branich, S.D.; Emmerson, P.T.; Ettian, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
Ci, Ebrlich, S.D.; Emmerson, P.T.; Ettian, C.V.; Erington, J.; Fabret, C.
Nature 390, 249-256, 1997
Nature 390, Nature 304, Nature 304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:299119; GB:AL039126; NID:g2635411; PIDN:CAB15034.1; PID:g2635540
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: virH:
A;Genome: plasmid
C;Superfamily: Agrobacterium plasmid cytochrome P450 pinFl; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein
F;366/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٠.
م
                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Mesiduse: 1-419 «KD»
A;Cross-references: GB:Arc08690; PIDN:AAL46386.1; PID:g17744179; GSPDB:GN00189
A;Experimental source: strain CS® (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 LLGTDPRIRQIETELML-----NRGVTRGAVFDLIRYSMLFSNGEVHVKRRSA---FAK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFGERNVVVTEGDLKKVLDGCAP-LTRFTNKLRTFGRTFTEAYVDFCIAYKHKLPQLNAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 TFAFR------MIDALRPEITKLTEHLWJDVPRVDD--FDFAEMYASKLPALTIA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SYLAADFLGTCPKLSELQ------QSRKM-- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 LNGVDKKLLSAEVEKMLVQKGAPNEGIE--VVFGLLLYALAARTTSPKVQRADSDVIFSN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-527 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 LNGVDKKLLSAEVEKMLV---QKGAPNEGIEVVFGLLLYALAARTTSPKVQRADSDVIFS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.8%; Score 87; DB 2; Length 527; Best Local Similarity 26.9%; Pred. No. 3.9; Matches 47; Conservative 24; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.1%; Score 90; DB 2; Length 419; Best Local Similarity 25.1%; Pred. No. 1.5; Matches 52; Conservative 26; Mismatches 71; Indels
A; Reference number: AB2577; MJID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: phosphoenolpyruvate carboxykinase (ATP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFLSCYLKAVREEGTL--SPIEEIMQL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 -FASMY -- ALKTEGGVVNTPVSNLRQL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 AELGIPAED-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::
::
                                                           A; Accession: AD3246
```

165

ಕ್ಷ ò g

ò

g े Db

ਨੇ

C; Genetics:

ò a à g ò dC ò a

str

```
A/Accession: G7501
A/Status: preliminary
A/Noiceule type: DNA
A/Noiceule type: DNA
A/Status: 1-447 «KAW»
A/Cross-references: GB:AJ48283; GB:AJ096836; NID:G5457433; PIDN:CAB49062.1; PID:e15149
C/Senetics: Cource: strain Orsay
C/Senetics: Dpp; PAB0087
C/Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE000348; GB:U00096; NID:g1788975; PIDN:AAC75675.1; PID:g1768980
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: 216465
A;Reference number: 108639
A;Ression: 1729 PUU>
A;Residues: 1-729 PUU>
A;Ressidues: 1-729 PUU>
A;Resperimental source: strain kl2, substrain MG1655
A;Experimental source: strain kl2, substrain MG1655
B;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rese, D.J.; Mau, B.; Shao, Y.
A;Reference number: A64720; MUD:97426617; PMID:9278503
A;Reference number: A64720; MUD:97426617; PMID:9278503
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
         R;anchymcus, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome
A;Reference number: A75091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 ARLPSTPETIYGIGSITKSFTALAIMKLVEEGGLS--LDD--PVEKFVNIKLRPFGEPVT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----YVDFCIAYK--HKLPQLNAAAELGIPAEDSYLAA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 KLESFIVEKMAERK-VPGISISII-------KDGDVVYAKGFGYRNVE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Escherichia coli
C;Date: 1.-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 01-Mar-2002
C;Accession: T08639; E65041
R;Plunkett, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----VVTEGDLKKVLDGCAPLTRFTN-KLRTFGRTFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 RTTSPKVQRADSDVIFSN---SFGERNV--VVTEGDLKKVLDGCAPLTRFTNKLRTFGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 ESYSEYLK----NJIDYARQWISEGEKRTLSIALMNDLKLI------TN---TRGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ELMSDSNLSNLVI--TDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 KLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKVQRADSDVIFSNSFGERNV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 22.4%; Pred. No. 8.1;
Matches 41; Conservative 31; Mismatches 64; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.7%; Score 86; DB 2; Length 447; 26.0%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein b2627 - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 EAYVDFCIAYKHKLPÇLNAAAEL -- GIPAEDSYL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---VHHLLTHSGIPSLGYAEAFIDGMVGGDNWL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 26.0%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-729 < BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 FTEA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 57 min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                φ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable beta-lactamase (EC 3.5.2.6) PAB0087 - Pyrococcus abyssi (strain Orsay) N;Alternate names: penicillin-binding protein homolog
C;Species: Pyrococcus abyssi
C;Date: 20-Aug_1999 #sequence_revision 20-Aug_1999 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                              137 SEQPNMFKSYTARLKGIVGDKKAMEIINNAFVVVSAGPNDFILNYYEIPSRALEYPFISG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TISPKYQRADSDVIFSNSFGERNVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 YQDFILKRLENFVRELYSLGVRNVLV--GGLPPX--GCLPI-HYTAKFRNIFRFCLEHHN 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DECIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALK-TEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 KDSVLYNEKLQNLJPQIEASJPG-SKFLYADVYN--PRYEMIQNPSK-----YGFKETKR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 GHSHPVFSGDRVHEFAMKLAGAIYMEVQQAGGGIMFTIN----KTREASEQDLRKDFEELA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLIRFINKLRIFGRIFTEAYVDFCIAYKHKLPQLN--AAAELGIPAEDSYLAADFLG--T 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 -----KKMLRSGTTTLEAKSGYGLNVDAEKKMLRVLATENPNIPLE---VSATFCGAHA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Residues: 1-445 <LAT>
A.Gross-references: EMBL:U13019; PIDN:AAC24449.1; GSPDB:GN00021; CESP:T12A2.1
A.Experimental source: strain Bristol N2; clone 712A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MELMSDSNLSNLVITDAS-----SLNGVDKKLLSAEVEKMLVQKGAPNEGIEV---- 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 ----- VF-GLLLYALA---ARTTSPKVQRADSOVIFSNSFGERNVVVTEGDLKKVLDGCA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypochetical protein T12A2.1 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Accession: T34352 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 #stateille, P. Submitted to the EMBL Data Library, March 1996 #submitted to The sequence of C. elegans cosmid T12A2. A.Reference number: Z21511 A.Reference number: Z21
                                                                                                                                                                                                                                                                                                          7 SNLSNLVITDASSLNGV--DKKLLSAEVEKMLVQKGAPNEGI----EVVFGLLLYALAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 IKILNDSSNSLVILVDTNGKFSYIGNLNGAENKLKGEGVEMENLKIIDSSNGGIAIPGFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 3
A;Introns: 33/3; 117/3; 146/3; 202/3; 250/2; 297/3; 371/1; 407/2
                                                                                                                                       Length 360;
                                                                                                                              Query Match 8.7%; Score 86; DB 2; Length 360
Best Local Similarity 26.5%; Pred. No. 2.9;
Matches 49; Conservative 23; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 VPKGSTEYEQTRXICEELIPKIEDEKRNGGLKN--VENI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 CPKLS-ELQQSR----KMFASMYALKTEGGVVNTPVSNL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

8.7%; Score 86; DB 2;
Best Local Similarity 24.7%; Pred. No. 3.8;
Matches 54; Conservative 41; Mismatches 8
                                          C, Superfamily: myrosinase-associated protein MyAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 GVVNT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: CESP:T12A2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: G75201
A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100
```

RESULT 14 G75201

ò ΩD ò Dp. તે ΩĐ ે a

90 S

15: DFL 153 | | 684 DLL 686

q

Search completed: November 7, 2003, 14:50:22 Job time : 23 secs

Run

rhizobium i odontella s

P529277 P54489 P544289 P549530 P549530 O358374 Q35874 P550234 C65015

emericella

mus musculu

rhodobacter schizosacch bacillus an archaeoglob arabidopsis

vibric algi trifolium r

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                    Citrus tristeza virus (isolate T36) (CTV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94160579; PubMed=8116253; Pappu S.S., Hilf M.E., Pappu H.R., Karasev A.V., Anderson E.J., Pappu S.S., Hilf M.E., Febres V., Eckloff R.M.G., McCaffery M., Boyko V., Gowda S., Dolja V.V., Koonin E.V.; McCaffery M., Boyko V., Gowda S., "Nucleotide sequence and organization of eight 3' open reading frames of the citrus tristeza closterovirus genome."; Vixology 199:335-46(1984).

Vixology 199:335-46(1984).

**RESULT OF POST-TRANSLATIONAL PROTEOLYSIS AT SITES APPROXIMATIVELY IZ TO 15 AND 26 AA FROM THE N-TERMINUS RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 27-38.
MEDINE-91237334; PubMed=2033386;
Sekiya M.E., Lawrence S.D., McCaffery M., Cline K.;
Molecular cloning and mucleotide sequencing of the coat protein gene of citrus tristeza virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 SSVNLHIDPTLITMNDVRQLSTQQNAALNRDLFLTIKGKHPNLFDXJXDFRIAMMLYRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 ARTTS-------PKVQRAD---SDVIF-SNSFGERNVVVTEGDLKKVLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 SSLN-GVDKKLLSA-EVEKMLVQKGA--------PNEGIEVVFGLLEYALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.6%; Score 125; DB 1; Length 223; 25.9%; Pred. No. 0.30025; ive 33; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 AA; 24909 MW; 00493F3D330220BB CRC64;
                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                     223 AA
                                                                                                                                                  ALIGNMENTS
PEPT STRPY
TKT RHOSH
ORCI SCHPO
SLA2 BACAN
APSB EMENI
KAD RHILO
YC24 ODOSI
SATT MOUSE
                                                                                            U203_ARATH
PROC_VIBAL
AMYB_TRIRP
                                                                                   ARCFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U16304; AACS9630.1; -.
InterPro; IPR002679; Closter_coat.
Pfam; PF01785; Closter_coat; I.
                                                                                                                                                                                                                                                                                                                                                                            Gen. Virol. 72:1013-1020(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M76485; AAA42924.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56; Conservative
                                                                                                                                                                                                     STANDARD;
 407
657
7057
7057
1058
1058
1058
1058
1058
1054
1054
1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=31712;
                                                                                                                                                                                                                                                                                         Closterovirus.
                                                                                                                                                                                                                                                            Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coat protein.
                                                                                                                                                                                                     CTV36
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
                                                                                                                                                                                T 1
CTV36
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                    yarrowia li
bacilius su
escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                              Q00686 citrus tris
P14605 schizosacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P57478 buchnera ap
Q8eyv8 l arginine
Q8uj94 agrobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rhizobium m
rhizobium s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         brucella me
brucella su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thermoanaer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       borrelia bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ພາກs ໝາຍcrຼາກ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lactocccus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          psendomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bradyrhizob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methanococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rhodopseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synechocyst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agrobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eynechococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               wiggleswort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         schizosacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eptospira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    salmonella
                                                                       ; Search time 17 Seconds (without alignments) 547.723 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rhizobium
                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                    1 MELMSDSNLSNLVITDASSL........GGVVNTPVSNLRQLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                            P54418
P52126
Q9znh4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            081558 051558 051558 055497 055497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P24466
Q3rei2
P43085
P55610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9cgm8
P31052 |
Q988p7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9d322
Q99840
Q99840
P52788
Q50725
                                                                                                                                                                                                                                                                                                                                                                                                                                         P14605
Q92389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       057639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2825j9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              088501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9shi1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P13440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28ye41
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                            of hits satisfying chosen parameters:
                                                                                                                                                                                         127863 segs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y175_METJA
HIS8_SALT:
PURA_WIGBR
                                                                                                                                                                                                                                                                                                                                                                                                                            COAT_CTV36
CYAA_SCHPO
AXP_YARLI
PPCK_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPCK FUSNN
PPCK RHIME
Y4PA RHISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRE_LACLA
DLD2_PSEPU
HIX2_RHILC
CAN6_RAT
IF2C_ARATH
PPCK_BRAJA
ARGE_LEPBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMYI_SCHPO
SPSY_HUMAN
YYOO_MYCTU
                                                                        7, 2003, 14:45:43
                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YFCK_ECOLI
PPCK_RHOPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARGJ_LEPIN
PPCK_AGRTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LACLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BRUNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNY3
                                                    sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGRTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNP7
                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACKA 1
LON2 1
SPSY 7
OTCA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPCK
PPCK
                                                                                                                                                                                                                                                                                                                                                                                                          Ωï
                                                   - protein search, using
                                                                                                                                                                                                                                  seq length: 0
seq length: 2000000000
                                                                                                                US-09-613-486-15
                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                                                                                                                                                                                                                           SwissProt_41:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    November
                                                                                                                                                          BLCSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ~ 00000ncc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.5
76.5
76.5
76.5
75.5
75.5
75
                                                                                                                                                                                                                                                                                                                                                                                                                             74.5
74.5
74.5
74.5
                                                                                                                Title:
Perfect score:
                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                             Total number
                                                                                                                                                                                                                                  Minimum DB
Maximum DB
                                                  OM protein
                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                      Sequence:
                                                                                                                                                                                         Searched:
                                                                        o
                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
```

38 88 98

64;

N

CYAA SCHPC

g

g 3

à

```
CATALYTIC ACTIVITY: ATP = 3','5'-cyclic AMP + diphosphate. COFACTOR: Binds 1 magnesium ion per subunit (By similarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IRR003591; LRR typ.
InterPro; IPR001932; PP2C-like.
InterPro; IPR001932; PP2C-like.
InterPro; IPR00189; RA_domain.
Pfam; PF00211; guanylate_cyc; 1.
Pfam; PF00481; PP2C; 1.
SWART; SX00349; LRR TYP; 1.
SWART; SX00349; LRR TYP; 1.
SWART; SX00349; LRR TYP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        GenedB SPombe; SPBC19C7.03; -.
InterPro; IPR001054; G cyclase
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL023859; CAA19571.1; -. PIR; A33988; A33988.
                                                                                                                                                                                                                                                                                                                                               EMBL; M26699; AAA35284.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 24.7%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                  M24942; AAA35301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380
403
427
475
475
524
547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  928
1008
1277
1337
1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Magnesium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          Geneba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
      검
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINES-1844401; PuchMed=11859360; Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Bodovos V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Bodovos V., Brown D., Bowman S., A., Brocks W., Brown D., Bowman S., A., Brocks W., Brown D., Bowman S., A., Brocks W., Brown D., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamilin N., Harris D., Hidagog J., Hodgson G., Holroyd S., Homesy T., Howarth S., Hutcher E.J., Hutt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Munghy L., Nibert D., Jodell C., A., Mooney R., O'Neil S., Mondari K., Muthphy L., Nibert D., Odell C., Router S., Saunders D., Seeger K., Sharp S., Stevens K., Arylor R., Simmonda M., Squares S., Squares S., Stevens K., Arylor R., Stevens M., Marlen S., Stevens R., Maish S., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Robel C., Fuchs M., Lehrach H., Reinhardt R., Pohl T.M., Berr P., Zimmermann W., Wedder H., Reinhardt R., Purnelle B., Lehrach H., Reinhardt R., Purnelle S., Lehrach H., Raibert H., Marbut R., Lucas M., Rochet M., Gallardin C., Hunt C., Moore K., Hurst S., Langar B., Berr P., Zimmermann W., Medler H., Raibert H., Bellice S., Sharketrong J., Forsburg S.L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Arthegenome sequence of Schizosaccharomyces pombe.", The genome sequence of Schizosaccharomyces pombe.", Purnell B., Langar B., Bellick B
                                                                                  99 APLTRFTNKLRFGRTFTEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPK 158
MEDLINE=89945533; Puched=2669944; Yamawaki-Kataoka Y., Tamaoki T., Choe H.-R., Tamaka H., Kataoka T., "Ademylate cryclases in yeast: a comparison of the genes from Schizosaccharomyces pombe and Saccharomyces cerevisiae."; Proc. Natl. Acad. Sci. U.S.A. 86:5693-5697(1989).
                                                                                                                                                                                                                                                                                                                01.APR-1990 (Rel. 14, Created)
01.APR-1990 (Rel. 14, Last sequence update)
15.SEP-2003 (Rel. 42, Last annotation update)
Adenylate cyclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Plays essential roles in regulation of cellular metabolism by catalyzing the synthesis of a second messenger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=90046723; PubMed=2682634;
WOUNG D., Riggs M., Field J., Vojtek A., Broek D., Wigler M.;
"The aderylyl cyclase gene from Schizosaccharomyces pombe.";
Proc. Nati. Acad. Sci. U.S.A. 86:7989-7993(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                   159 LSELQOSRKMFASMYALKTEGGVVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                      CYRI OR SPBC19C7.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=4896
                                                                                                                                                                                                                                                                               SCHPO
                                                                                                   133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     cyclase)
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 LLSAEVERMINQKGAPNEGIEVVFGLLLYALAARTTSPKVORADSDVIFSNSFGERNVVV 86
-:- COFACTOR: Binds I magnesium ion per subunit (By similarity).
-:- ENZYME REGULATION: In contrast to yeast cyclase, S.pombe cyclase is not likely to be regulated by RAS proteins.
-:- SIMILARITY: Belongs to the adenylyl cyclase class-3 family.
-:- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
-:- SIMILARITY: Contains 1 PP2C-like domain.
-:- SIMILARITY: Contains 1 Ras-associating domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyase; Repeat; Leucine-rich repeat; cAMP biosynthesis; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.3%; Score 92; DB 1; Length 1692; 24.7%; Pred. No. 3.1; ive 26; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 MAGNESIUM (BY SIMILARITY).
80 MAGNESIUM (BY SIMILARITY).
190333 MW; D137CBE8770A8655 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAS-ASSOCIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE, PS50125, GUANYLATE_CYCLASES_2, 1.
PROSITE, PS50200, RA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRR 4.

LRR 5.

LRR 6.

LRR 9.

LRR 9.

LRR 10.

LRR 11.

LRR 12.

LRR 12.

LRR 14.

LRR 16.

LRR 17.

LRR 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC
```

۸

```
164 ----- OSRKMFASMYALKTEGGVVNTPVSN 188
                                                                                                                                                                                                             311 FTYNFSGKEITVTGHDIAIPGNAVNSNVDS 340
                                                                     131 PQL----NAAAELGIPAEDSYLAAD----FLG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98644033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-165 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCKA OR
                                                                                                                                                                                                                                                                                RESULT
                                                                ò
                                                                                                             ac
                                                                                                                                                              ò
                                                                                                                                                                                                        ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL cutstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                TIMDI - - - - GABULRKFSEKKITANLDISRSNLEVIPVKIYPYAHELISLNVSHNLSLD 443
                   TEGDLKKVLDGCAPLTRFTNKLRT----FGRTFTBAYVDFCIAYKHKLPQLNAAAELGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDNAVIGGA-----SAPGFKFGVNSGDLSSGGFSMVFGIGVNSDASTSISAQLGKSGEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDASSLNGVDKKLLSAEVERMLVQKG-APNEGIEVVFGLLLYALAARTTSPKVQRAD--S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATION PEPTIDE (POTENTIAL).
ACID EXTRACELLULAR PROTEASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N.LINKED (GLCNAC. .) (POTENTIAL).
N.LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Yarrowia lipolytica (Candida lipolytica).
Eukaryota: Fungi: Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=148;
MEDLINE=97039861; PubMed=8885407;
Young T.W., Wadeson A., Glover D.J., Quincey R.V., Butlin M.J.,
                                                                                                                                             -----LPLDFMERCVKLKRLDISNN-----LRSPRG---KPITALRQL 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The extracellular acid protease gene of Yarrowia lipolytica:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF3002b; asp, ...
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; 1.
Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal.
Hydrolase; Aspartyl protease; POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.0%; Score 89.5; DB 1; Length 397;
                                                                                                             143 AEDSYLAADFLGTCPKLSELQQSROMFASMYALKTEGGVVNTPVSNLRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LINKED (GLCNAC. . .) (PC
BD678814B4B8984F CRC64;
                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acid extracellular protease precursor (EC 3.4.23.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence and pH-regulated transcription.";
Microbiology 142:291:2921(1996).
-- SUBGELLULAR LOCATION: Secreted.
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Mismatches
                                                                                                                                                                                                                                                                                397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro, IPR001969, Aspprotease site.
InterPro, IPR001461, AspproteaseAl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42081 MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X97068; CAA65778.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314
397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; A01.036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
264
93
303
88
                                                                                                                                                                                                                                                                                AXP_YARLI
Q92389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
ACT SITE
ACT SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
                                                                  389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
```

THE PROPERTY OF THE PROPERTY O

72 DVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTE-AYVDFCIAYKHKL 130

Best Loca Matches

g

ò

```
A Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Baroriss P.L., Brans A., Braun M., Brignell S.C., Bron. S., Brouilser L., Brans A., Braun M., Brignell S.C., Bron. S., Brouilser L., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., R. Britz C., Fujita M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., R. Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., R. Entizon M., Fabret C., Ferraria E., Foulger D., Ramerson P.T., Rabert D., Goffeau A., Golightly E.J., Grandi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A., R., Holseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A., Guiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Krogh S., Kuman D., Kashara Y., Koningstein G., Krogh S., Kuman D., Kashara Y., Koningstein G., Krogh S., Kuman D., Kashara Y., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Anderina N., Mellado R.P., Mizuno M., Mosetl D., Navai S., Noback M., R. Monoe L., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Peresecan E., Pulic P., Purnelle B., Rapoport G., Rey M., Septoni S., Scholei B., Rapoport G., Rey M., Sator J., Serror P., Soficule F., Schleich S., Schroeter R., Scoffone F., Schleich S., Schroeter R., Scoffone F., Takagi T., Takamaru K., Takemaru K., Rabeuchi M., Tamakoshi A., Tanamanchi M., Vannanck T., Weitzerneger T., Amanute R., Wandute R., Wandut
-----TCPKLSELQ
                        MEDLINE=98048467; PubMed=9387221;
Lapldus A., Galleron N., Sorokin A., Ehrlich S.D.;
"Sequencing and functional annotation of the Bacillus subtilis genes
in the 200 kb rrnB-dnaB region.";
Microbiology 143:3431-3441(1997).
                                                                                                                                                                                                                                                                        PPCK_BACSU STANDARD; PRT; 527 AA.

92418; 033304;
01-6CT-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
Phosphoenolypruvate carboxykinase (APP) (BC 4.1.1.49) (PEP earboxykinase) (Phosphoenolpyruvate carboxylase) (PEPPCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=168 / PY79;
MEDLINE=96345628; PubMed=8755891;
Yocum R., Perkins J.B., Howitt C.L., Pero J.;
```

```
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFL 153
   complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHOPA
                                                                                                                                                                                                                                                                                                                                                                                                      115
                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
                                                                                                                                                                                                                                                                   Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPCK RHO
Q9ZNH4;
               Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPCK_RHOPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                    D,
                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                        Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD.
                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 LSGTGKTTJSADADRKLIGDDEHGWSDTGVFNIEG-GCYAKCIHLSEEK----EPQIFNA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 IRFGSVLENVVVDED-----ATREANYDDSFYTENTRA-----AYPIHMINNI 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSFGE--RNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIAYK-HKLPQL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                    76
            adenosylmethionine synthetase from Bacillus subtilis.";
J. Bacteriol. 178:4604-4610(1996).
-!- CATALYTIC ACTIVITY: ATP + oxalcacetate = ADP + phosphoenolpyruvate
                                                                                                                                                                                                                                                     -!- PATHWAY: Rate-limiting gluconeogenic enzyme.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [ATP]
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNGVDKKLLSAEVEKWLV---OKGAPNEGIEVVFGLLLYALAARTTSPKVQRADSDVIFS
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 NAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKM--FASMYALK---TEGGVVN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 VTPSMAGHPSAIVFLTADAFGVLPPISKLTKEQVMYHFLSGYTSKLAGTERGVTS 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=KI2 / MG1655,
MEDLINE=97426617; PubMed=92785C3;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                      8.8%; Score 87; DB 1; Length 527; 26.9%; Pred. No. 2.2;
  ď
                                                                                                                                                                                                                                                                                                                                                                                                                             70; Indels
"Clouing and characterization of the metE gene encoding
                                                                                                                                                                                                                                                                                                                                                        ATP (BY SIMILARITY).
L -> S (IN REF. 3).
ESSIEEC80201E666 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yfjk.
                                                                                                                                                                                                                                                                                                                                                                                                                             24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         729
                                                                                                                                                                                                           EMBL; AF008220; AAC00377.1; -.
                                                                                                                                                                                                                                                                                                                                                                               527 AA; 58300 MW;
                                                                                                                                                                                                                     EMBL; Z99119; CAB15034.1; -. EMBL; U52812; AAB17065.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 6.84
Best Local Similarity 26.97
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                            PIR; F69673; F69673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFJK_ECDLI
ID YFJK_ECOLI
AC P52126;
                                                                                           family.
                                                                                                                                                                                                                                                                                                                                                          NP BIND
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/anncuncel or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 RTTSPKVQRADSDVIFSN---SPGERNV--VVTEGDLKKVLJGCAPLTRFTNKLRTFGRT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTEA------YVDFCIAYK--HKLPQLNAAAELGIPAEDSYLAA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     624 LPKVLSLMEDVVKHHAVKRGIRSKVDYTHVKLAFESFHLPPGVNALEEIGIPICTLHRLV 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          palustris no. 7 phosphoenolpyruvate carboxykinase gene.";
J. Bacteriol. 181:2689-2696(1999).
-!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [ATP]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ELMSDSNLSNLVI--TDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 ESYSEYLK---NOIDYARGWISEGEKRILSIALNNDLKLI------TN---TPGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inui M., Nakata K., Roh J.H., Zahn K., Yukawa H.;
"Molecular and functional characterization of the Rhodopseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
NCBI_TaxID=1076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PE. carboxykinase) (PEDCK).
genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., SEQUENCE OF 1-12, AND DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR00165v, .....
Pfer; Pr00271; helicase C; 1.
SNART; SW00480; DEXDC; 1.
SNART; SW00490; HELICc; 1.
Hypothetical protein; Complete proteome.
Appothetical protein; Complete proteome.
- or c; DB 1; Lengt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.6%; Score 85.5; DB 1;
22.4%; Pred. No. 4.4;
tve 31; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-EBS-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase [ATP] (EC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   537 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99235744; PubMed=10217755;
                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000348; AAC75675.1; -.
PIR; T08639; T08639.
EcoGene, EG13197; Yf2.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Hellcase
                                                                                                                                                                                                                                                                                                                                                     EMBL; U36840; AAA79796.1; -.
                                    277:1453-1474 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodopseudomonas palustris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMIS, outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way wordfited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright, It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBS outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 -STRFGAVLENVVLGDIDRKPDFDDGSK----TENTRS-----AYPLESIP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 NASLIGRAGOPKNVVMLAADDAFGVMPPIAKLIPAQAMYHFLSGYTAKVAGTERGVTEFIP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 LSGTGKTTLSADPNRTLIGDDEHGWGKDGVFNFEGGCYAKCIKLSAENEPEIYAA---- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 INGVDXKILSAEVEKMLVQKGAPNEGIEVVFGLL--IYALAARTTS---PKVQRADSDVI 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 FSNSFGE--RNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIAYK-HKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 QINAAABLGIPAEDSYLAADFLGTCPKLSELQQSRKY--FASMYALK---TEGGVVN-TP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Tokyo 1998;
BDDLINE=20445131; PubXed=10993377;
Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                     HSSP; P22259; IAU2.
R HAMAP; MF_00453; -; 1.
R InterPro; IPR001272; PEPCK ATP.
R Prodom; P0004723; PEPCK ATP.
DR Prodom; TIGR00224; pcKa.1.
DR PROSITE; P805523; PEPCK ATP; 1.
DR PROSITE; P805523; PEPCK ATP; 2.
DR PROSITE; P805523; PEPCK ATP; ATP; PALSE NEG.
KW Gluconeogenesis; Lyase; Decarboxylase; ATP-binding.
ATP (BY SIMILARITY).
236. 243.
ATP (BY SIMILARITY).
237. 58773 MW; 9BF0ECICEDIC9EA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.5%; Score 84; DB 1; Length 537; 26.7%; Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NACUTE 407:81-86(2000).
-!- SIMILARITY: BELONGS TO THE TLDD/PMBA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP001119; BAB13101.1; -.
InterPro; IPR002510; PmbA_TldD.
                                                                                                                                                                                                            EMBL; AB015618; BAA34956.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buchnera sp. APS.";
Nature 407:81-86(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TldD protein homolog. TLDD OR BU398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=118099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLDD_BUCAI
P57478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \stackrel{>}{\circ}
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                           305 KNORGSLSIDJEGTPGOKNILIENGILKKYMQDKLNARLMGVKSTGNGRRESYSCLPMPR 364
                                                                                                                                                                                                                                                       104 FINKLRIFGRIFTEAYVDFCIAYKHKLPQLNAAABIGIPAEDSYLAADFLGTCPKLSELQ 163
                                                                                                                                                                                                                                                                                              365 MTN-----YAVNFSG---GOVDIT 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
MEDLINE=22598143; PubMed=12712204;
MEDLINE=22598143; PubMed=12712204;
MEN S.-X.; Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Yong H., Lu G., Lu L.-F., Jiang H.-Q., Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Man M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- FUNCTION: Catalyzes two activities which are involved in the cyclic version of arginine biosynthesis: the synthesis of acerlygiutamate from glutamate and acetyl-CoA, and of ornithine by transacetylation between acetylornithine and glutamate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- MISCELLANEOUS: Some bacteria possess a monofunctional argJ, i.e.,
capable of catalyzing only the fifth step of the arginine
                                                                                                                                                                     -GCAPLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-532-2003 (Rel. 42, Created)
15-532-2003 (Rel. 42, Last sequence update)
15-532-2003 (Rel. 42, Last sequence update)
Arginine biosynthesis bifunctional protein argJ [Includes: Glutamate N-accryltransferase]
(Cornithine deceyltransferase)
(EC 2.3.1.1) (N-accrylase) (OATase); Amino-acid accryltransferase
biosynthesis bifunctional protein argJ alpha chain; Arginine ArgJorn (ArgJornal protein argJ beta chain; Arginine ArgJoR (OR 14405)
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
--- CATALYTIC ACTIVITY: N(2)-acetyl-L-ornithine + L-glutamate = L-
ornithine + N-acetyl-L-glutamate.
--- CATALYTIC ACTIVITY: Acetyl-CoA + L-glutamate = CoA + N-acetyl-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jeptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glutamate.
--- PATHWAY: Arginine biosynthesis, first step.
--- PATHWAY: Arginine biosynthesis, fifth step.
---- SUBUNIT: Heterotetramer of two alpha and two beta chains (By
                                                                                                                                45,
                                                                                      483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unique physiological and pathogenic features of Leptospira
                                                                                                                                Inders
                                                                                      Length
                        Complete proteome.
SEQUENCE 483 AA; 52977 MW; A05CE98518720EBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interrogans revealed by whole-genome sequencing.";
Nature 422:888-893(2003).
                                                                                                                                                                                                                                                                                                                                                                                437
                                                                                                                                                                                                                                                                                                                                           164 CSRKMFASKYALKTEGGVVNTPVSNLRQLGR-REVM 198
                                                                               1.arity 20.5%; Pred. No. 4.1; Conservative 26; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                 402 SGKFVFSTSEAYLIKNGKIVTPIKNTTLIGSGLEVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the arg. family.
                                                                                                                                                                       65 KVORADSDVIFSNSFGERNVVVTEGDLKKVLD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
Pfam; PF01523; PmbA_TldD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   losynthetic pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                   Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARGU LEPIN
QBEYVB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEPIN
  SOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                        5
C
                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                        à
```

```
the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 LQIYPG----TLPVKEANPETLKKLSEYLKNYTEISLNVVLNVGTISMKFWGC----- 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 TKLIELTISGAKSEAQARKIGKSILNSPLVKTAIYGGDPNWGRLIMAVGKVFDEPIPFEG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IEVVFGLLLYALAARTTSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAP1TRFT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN ARGJ ALFHA CHAIN (BY SIMILARITY).
ARGJINNE BLOSVYTHEBIS BIUNCTIONAL
PROTEIN ARGJ BETA CHAIN (BY SIMILARITY).
CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21608550; Pubmed=11743193; Monks D.E., Kitajima J.P., Mood D.W., Setubal J.C., Rull R., Monks D.E., Kitajima J.P., Mood D.W., Setubal J.C., Rull R., Monks D.E., Kitajima J.P., Mood D.W., Zhou Y., Chen Y., Zhou Y., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Woo L., Chapman P., Clendenning J., Dearherage G., Glilet M., Jarnt C., Kutyyavin T., Levy R., Im.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Palmieri A., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry X., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      ARGININE BIOSYNTHESIS BIFUNCTIONAL
                                                                                                                                                                  EMBL; AE011564; AAN51303.1; -.
HAMAP; MF 01106; -; 1.
InterPro; TPR002813; ArgJ.
Pfam; PF01960; ArgJ; 1.
ProDom; PD034193; ArgJ; 1.
ProDom; TIGRO0120; ArgJ; 1.
Argjinne biosynthesis; Miltifunctional enzyme; Transferase; Acyltransferase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).
PCKA OR ATU0035 OR AGR_C 56.
Sagrobacterium tumefaciens (strain CS8 / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria; Rhizobiales;
Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.1.1.49) (PEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.4%; Score 83; DB 1; Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8A525296D0AD7C2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase (ATP) (EC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 21.3%; Pred. No. 3.4; nes 29; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 AA; 41445 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----- 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 NKLRTFGRTFTEAYVD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         178
                                                                                                                                                                                                                                                                                                                                                                                                                                                               385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179
                                                                                                                                                                                                                                                                                                                                                                                                                                                            179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPCK AGRTS
08UJ94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESULT 9
PCK_AGRT5
                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
   O OOOOOKKKKKKKKKK
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 LSGTGKTTLSADPARTLIGDDEHGWGEHGIFNFEGGCYAKAIKLSSEAEPEIYAA---- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 FSNSFGE--RNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIAYK-HKLP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP, MF 00453, 11.

InterPro; IPR01272; PEBCK ATP.
Pfam, FF01293; PEBCK ATP.
TIGR0021293; PEBCK ATP.
TIGRAMS; TIGR00214; PCA; 1.
PR051TE; PS0512; PEBCK ATP; 1.
PR051TE; PS0512; PEBCK ATP; 1.
PR051TE; PS0512; PEBCK ATP; 1.
ROSITE; PS0512; PEBCK ATP; 1.
ROSITE; PS0512; PSECK ATP; 1.
ROSITE; PS0512; PSECK ATP; 1.
ROSITE; PS0512; PSECK ATP; 1.
ROSITE; PS0512; PS124; PS124;
                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: Rate-limiting gluconeogenic enzyme.
-!- SDSCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [ATP] family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 INGVDKKILSAEVEKMLVQKGAPNEGIEVVFGLL--LYALAARTTS---PKVQRADSDVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 ÇLNAAAELGIPAEDSYLAADFLGTCPKLSEL--QQSRKMFASMYALK---TEGGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dong W., Yang J.,
X., Ma Y., Ling L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz Flandsan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., "Genome Sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens 658 ";
Science 294:2121-2328(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (BY SIMILARITY). 6F90B8F484C86A5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN=MB4 / JCM 11007;

MEDLINE=21992816; PubMed=11997336;

Chen Y., Xue Y., Xu Y., Laxi X., Xuan Z., Hu S., Dong Chen Y., Xue Y., Xu Y., Laxi X., Huang L., Dong X., Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan H., Chen R., Wang J., Yu J., Yang H.;

Genome Res. 12:689-700(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 -TNRFGTVLENVVLDESRVPDFNDN--SLTENTRS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ACKA OR TEB1481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoanaerobacteriaceae; Thermoanaerobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.9%; Pred. No. 5.1; ative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.4%; Score 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE008978; AAL41066.1; ALT INIT.
EMBL; AE007946; AAK85859.1; ALT INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoanaerobacter tengcongensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536 AA; 57882 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sest Local Similarity 26.98
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACKA_THE
Q8R9V4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACKA_THETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SO THE TRANSPORT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
```

```
InterPro;
                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPMSY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fat ches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
    dC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 င်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BMED outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions at long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----KLRIFGRIFIE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 GGEYFTDSVLIDDEVIKK-LEDČIJLAPLHNPANIEGIKACQQIMPGVPMVAVFDTAFHQ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KHKLPQINAAAELGIPAEDSYLAADFLGTCP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 TMPDYAYIYPIPYEYYEKHRIRRYGPHGTSHKYVSMRAABILGRPIEELKIVTCHLGNGA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GINDS:LTHQAEGKEKVKIQREXKNHKEAIQLVLEVLVDKEIGV:KOMKEIDAVGHRVVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraer C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougherty B., Tomb J.-F., Fletschmann R.D., Richardson D., Pertson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald J., Artiach P., Sowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 GVDKKLLSAEV---EKMLVQKGAFN--EGIEVVFGLL1-YALAARTTSPKVQRADSDVIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
CATALYTIC ACTIVITY: ATP + acetate = ADP + acetyl phosphate.
                  -!- PATHWAY: Conversion of acetate to acetyl-CoA; first step. -!- SUBCELLULAR LOCATION: Cytoplasmic (3y similarity). -!- SIMILARITY: Belongs to the acetokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 401;
                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01075; ACETATE_KINASE_1; 1.
PROSITE; PS01076; ACETATE_KINASE_2; 1.
TAGNSTE1E PS01076; ACETATE_KINASE_2; 1.
TAGNSTE1E PS01076; ACETATE_KINASE_2; 1.
SEQUENCE 401 AA; 44361 WW; PD710642F1E019B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 SNSFGERNVVTEGDLKKVLDGC---APLIRFIN-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ATP-dependent protease ia homolog (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:580-586(1997).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.2%; Score 81.5; DB Best Local Similarity 19.3%; Pred. No. 5; Matches 40; Conservative 35; Xismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               813 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 KLSELQOSRKMFASMYALKTEGGVVNT 184
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00871; Acetate kinase; 1.
TIGRFAMs; TIGR00016; acka; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
MEDLINE=98065943; PubMed=9403685;
                                                                                                                                                                                                                                                                        HAMAP; MF G0020; -; 1.
InterPro; IPR00089C; Acetate_kin.
InterPro; IPR004372; Acka.
                                                                                                                                                                                                                                                      EMBL; AE013105; AAM24700.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 AYVDFCIAY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LON2 BORBU
051558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N2_BORBU
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  475 DESNVLPVTTANSLNGMSKPLLD-RMEIIKVEGYSYIEKLEIAKIFEIPSIIKESFEDKV 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 NLSN-LVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 Q-RADSDVIFSNSFGERNVVVTEG--JUKKVLDGCAPLTRFTNKLRTFGRTFTEAY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 YIRIEDDVIFNLI---RNYTMESGVRGLKRVL------TNLIRRLVRELLYEY 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Spermine synthase (EC 5.1.22) (Spermidine aminopropyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Mermazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
Strom T.M., Francis F., Lorenz B., Boeddrich A., Econs M.J.,
Lehrach H., Meitinger T.;
"Pex agene deletions in Gy and Hyp mice provide mouse models for
X-linked hypophosphatemia.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Diaphragm;
Nitranen K., Korhonen V., Janne J.;
"Nucleotide sequence of mouse spermidine aminopropyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.2%; Score 81.5; I
                                                                                                                                                                                                                                                                                                                                        IPRC03959; AAA_ATPase_centr. IPR003111; LON.
                                                                                                                                                                                                                                                                                                                                                                                               IPRC01984; Lon_endopep.
IPRC04815; Lon_fam.
                                                                                                                                                                                                                                                                                                               InterPro; IPR003593; AAA_ATPase
                                                                                                                                                                                                          EMBL; AEGG1162; AAC66962.1; -. PIR; D70176; D70176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 31.9
es 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PFC0004, AAA, 1.
Pfam, PF02190, LON, 1.
Pfam, PF05362, Lon C, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                   PIR; D70176; D70176
MERCPS; S16.UPW; -.
TIGR; BBC613; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPSY_MOUSE
ID_SPSY_MOUSE
AC_P97355;
```

α

```
NCBI_TaxID=358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pTiA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPXC_AGRTU
P24466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE SOUCH SERVICE STATES OF THE SERVICE SOUCH SERVICE 
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 FGRTFT-----EAYVDFCI-----AYKHKLPQLNAAAELGIPAEDSYLADF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 DGRLVEYDIDEVVYDEDSPYONIKILHSKQFGNIL-----ILSGDVNLAESDLAYTRAI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 MGSGKEDYTGKDVLILGGGDGGILCEIVKLKPKAVIMVEIDQMVIDGCKKYMR-----RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 CGDVLDNIRGDCYQVLIEDCIPVLKMYAKEGREFDYVINDITAVPISTSPEEDS--TWDF
                                         MEDLINE=98133937; PubMed=9467015;
Lovenz B., Francis F., Gempel K., Boeddrich A., Josten M., Schmahl W.,
Schmidt J., Lehrach H., Melinger T., Strom T.M.;
"Spermine deficiency in Gy mice caused by deletion of the spermine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 DKKLLSAEVEKMLVQKGAPNEGIEVV----FGLL:YALAARTTSPKVQRADSDVIFSNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------GERNWWTEGD-----LK------KVLDGCAPLTRFTNKLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76; Gaps
                                                                                                                                                                                                             synthase gene.";
Hum. Mol. Genet. 7:541-547(1998).
-!- CATALYTIC ACTUVITY: S-adenosylmethioninamine + spermidine = 5'-
methylthioadenosine + spermine.
-!- PATHWAY: BIOSYNTHESIS OF SPERMINE FROM SPERVIDINE.
-!- SIMILARITY: BELONGS TO THE SPERMIDINE/SPERMINE SYNTHASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JJJ-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ornithine carbamoyltransferase, anabolic (EC 2.1.3.3) (OTCase)
ARGF OR SLL0902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JGTCPKLS--ELQQSRKMFASMYALKTEGGVVN-TPVSNL--RQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRLILDLSMKVLKÇDGKYF -----TQGNCVNLTEALSLYEEQLGR 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SINDING TO DECARBOXYLATED SAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 AA; 41313 MW; DS49F319F51C43C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL TaxID=1148;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Pred. No. 6.1; 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:109490; Sms.
GO; GO:0008215; P:spermine metabolism; IMP.
Interpro; IFF001045; Sprainine synthase.
Pfam; PF01564; Spermine synth; 1.
PROSITE; PS01330; SPERMIDINE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.1%; Score 80; 22.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, Y09419; CAA70573.1; -. EMBL, A7031486; AA886631.1; EMBL, A7000008; CAA03919.1; EMBL, AJ000008; CAA03918.1; EMBL, AJ000008; CAA03918.1; JOINED. EMBL, AJ000009; CAA03918.1; JOINED. EMBL, AJ000009; CAA03918.1; JOINED. EMBL, AZ000092; CAA03918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT:
SEQUENCE OF 316-366 FRCM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 22.7*,
These 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA_SYNY3
OTCA_SYNY3
Q55497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 LNPSVIQVGRGEPIQDTARVLDRYIDILAVRTFKQTDLQTFADHA-----KYPIINALSD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 LSAEVEKMLVQKGAP-NEGI-----EVVFGLLLYALAARTTSPKVQRADSJVIFSNSFGE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 RNVVVTE-GDLKKVLDGCAPLTRFTNKL--RTFGRTFTEAYVDFCIAYKHKLPQLNAAAE
17 LTIEEMKSLLQLAADLKSGVLKPHCRKILGLLFYKASTRT---RVSFTAAMYQLGGQVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.0%; Score 79; DB 1; Length 308;
14.8%; Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-89213933; PubMed-2708311;
Kanemoto R.H., Powell A.T., Akiyoshi D.E., Regier D.A.,
Kerstetter R.A., Nester E.W., Hawes M.C., Gordon M.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGRO0658; orni carb tr; 1.
PROSITE; PS00097; CARBAMOŽITRANSFERASE; 1.
Arginine biosynthemis; Transferaes; Complete protecme.
SEQUENCE 308 AA; 33616 MW; C6CD2E4998592CFA CRC64;
                                                                                                                                                                                                                                                                                   -!- PATHWAY: Arginine biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-YAR.1992 (Rel. 21, Created)
01-YAR-1992 (Rel. 21, Last sequence update)
28-FEB-2033 (Rel. 41, Last annotation update)
Cypcohrome P450-pinF1, plant-inducible (EC 1.14.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 LGIPAEDSYLAADFLGTCPKLSELQQSRKMFASWYAL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----CQILADLOTIKECFGKLEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            422 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, P04391, TAKM.
InterPro, IPR306130, Asp/Orn_COtranf.
InterPro, IPR002292, Orn_carbtransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro; IPR006131; OTCace O. InterPro; IPR006132; OTCace P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D64006; BAA10847.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00185; OTCace; 1.
Pfam; PF02729; OTCace N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00100; AOTCASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S76000; S76000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
```

us-09-613-486-15.rsp

```
Search completed: 1
Job time : 18 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "atches
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ਨੇ
                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMEL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 --SFGERNVVVTSGDLKKVLDGCAP-LTRFT-----NKLRTFGRTFTEAYVDFCIAYK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 INGVDKKILSAEVEKMIVQKGAPNEGIE--VVFGLIJYALAARTISPKVQRADSDVIFSN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; MIJJS4; ALLES BERL; MIJJS4; ALLES BERL; MIJJS6; ALLES BERL; ALS 16F001128; Cytochrome_P450.

PERM; PR00667; p450; 1.

PRINTS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME_P450; 1.

Oxidoreductase; Monooxygenase; Electron transport; Heme; Plasmid.

Oxidoreductase; Monooxygenase; Electron transport; Heme; Plasmid.

METAL 369 189 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from Agrobacterium tumefaciens.";
J. Bacteriol. 171.2506.2512(1989).
-!- FUNCTION: NOT ESSENTIAL FOR VIRULENCE, BUT MAY BE INVOLVED IN THE DETOXIFICATION OF PLANT PROTECTIVE AGENTS AT THE SITE OF WOUNDING.
-!- INDUCTION: TRANSCRIPTONALLY ACTIVATED IN THE PRESENCE OF WOUNDED PLANT TISSUE AND BY PLANT PHENCLIC COMPOUNDS, SUCH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLGTDPRTRQIETELML - - - - - NRGVKAGAVFDFI - - - - - - - - - - DHSMLFSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 GETHGKRRSGLSKAFSFRMVEALRPEIAKITECLWDDLQKVDDF--NFTEMYAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kapatral V., Arderson I., Ivanova N., Reznik G., Los T., Lykidis A. Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Sozoa M., Walunas Y., Pusch G., Haselkorn R., Fonstein X., Kyrpides N., Overbeck R., "Genome sequence and analysis of the oral bacterium Fusobacterium
analysis of the plant-inducible locus pinf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 HKLPQLNAAAELGIPAED------SYLAADFLGTCPKLSELQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60; Indels
                                                                                                                                                                                         -!- SIMILARITY: Belongs to the cytochrome P450 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 -- CSRKM---FASMYALKT--EGGVVNTPVSNLRQ1 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 ADSGRRMRDDFLSRY-LKAVREAGTL-SPIEEIMQL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     527 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 79; 23.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21886394; PubMed=11889109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 23.6%
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusobacterium.
NCBL_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCKA OR FN1120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OBREI2;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EVML outstation. The European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as ing as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 LSGTGKTTLSADPNRKLIGDDEHGWCDKGIFNFEG----GCYAKCINLK-EESEFEIYRA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 NSFGE--RNVVVTEGDIKKVLDGCAPLTRFTNKLRTFGRTFT-EAYVDFCIAYKHKLPQL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 IKFGSLVENVVVD-----PITR---KIQYEDASITPNTRVGYPIDY---IPNA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9′
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AZOlvolo, ...

HANAR: Mr 20453; -; 1.

HANAR: Mr 20453; -; 1.

InterProj IPR001272; PEPCK ATP.

Prodom: P7014723; PEPCK ATP; 1.

TISPRAM: TIGRO0224; PEPCK ATP; 1.

TISPRAM: TIGRO0224; PEPCK ATP; 1.

PROSITE: PS00532; PEPCK ATP; ...

Gluconeogenesis: Lyase; Decarboxylase; ATP-binding; Complete proteome. arub

230 237 ATP (BY SIMILARITY).

F4055 MW; 275849FDF254AC01 CRC64;
J. Bacteriol. 184:2005-2018(2002).
-!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
                                                                                                      -:- PATHWAY: Rate-limiting gluconeogenic enzyme.
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [ATP]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 INGVDXXILSAEVEKMIV---QKGAPNEGIEVVFGLILYALAARTTSPKVQRADSDVIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 ELSGVGGIPKVVIFLTADSFGVLPPISRLSQEAAMYHFVTGFTAKLAGTELGV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 NAAABLGIPAEDSYLAADFLGTCPKLSELQQSRKM--FASMYALK---TEGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%; Score 79; DB 1
26.6%; Pred. No. 12;
tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   completed: November 7, 2003, 14:49:01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
```

Ę

tris tris tris tris

tris tris tris tris tris tris tris tris tris

tris

us-09-613-486-15.rspt

```
61 ITSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLIRFTNKLRIFGRTFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DPCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQOSRKMFASMYALKTEGG 180
                                                                                                                                                                                                                                  citrus tris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9dtf8 citrus to 010474 citrus to 080819 citrus to Q801919 citrus to Q80319 citrus to Q9pxt2 citrus to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grapevine leafroll-associated virus 2.
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MELMSDSNISNLVITDASSINGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLILYALAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTSPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WELMSDSNLSNLVITDASSINGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLIYALAAR
                                                                                            citrus de citrus
                                                                                                                                                                                                                                                                                                   citrus t
                                                                                                                                                                                                                                                                                                                                                                                                citrus
                                                                                                                                                                                                                                                                                                                                                                                                                                         citrus
                                                                                                                                                                                                                                                        citrus
citrus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       citrus
                                                                                                                                                                                                            citrus
                                                                                                                                                                                                                                                                                                                                                                          citrus
                                                                                                                                                                citrus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98264507; PubMed=9603345;
MEDLINE=98264507; PubMed=9603345;
Zhu H.Y., Ling K.S., Goszczynski D.E., McFerson J.R., Gonsaives D.;
Zhu H.Y., Ling K.S., Goszczynski D.E., McFerson J.R., Gonsaives D.;
"Nucleotide Sequence and Genome Organization of Grapevine Leafroli-
"Sociated Virus- are Similar to Beet Yellows Virus, the
Closterovirus Type Member.",
J. Gen. Virol. 79:1289-1298 (1998).
InterPro; IPR002679; Closter_coat.
Pfam. PF01785; Closter_coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                 099693
0997473
0997019
0997019
0997019
0997019
0997019
0997019
0997019
                                                                                                                                                                                                                                                                                                                                                                                                299196
099eg6
Q8v1p5
                                                                                                                                                                                                                                                                                                                                                  08jyu9
09pxs9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CBjyvc
Q9pxt1
                                                03bxc0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 AA; 21660 MW; 8ED85EF2EF1DFB03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                071213;
21-A3G-1998 (TrEMBLrel. 07, Created)
01-A3G-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 100.0%; Score 991; DB 12; Local Similarity 100.0%; Pred. No. 7.7e-89; les 198; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       C8V1P5
C8V1P5
C8V1P5
C9PTT1
C9DTF8
C1C474
C8B3R9
                   095770
095XT0
095XT0
095WW1
0957M3
098V1P7
0990N9
                                                                                                                                                                                                       P89948
Q990P1
Q9WID9
Q9IFW4
                                                                                                                                                                                                                                                                                                 006192
09PXT3
08JYU9
09PXS9
0991G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8JYU8
Q9FXT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      099AT6
    PRELIMINARY;
22 kJa coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=64003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Closterovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                         120.5
120.5
120.5
120.5
120.5
1120.5
1130.5
1118.5
117.5
117.5
116.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224.5
113.5
111.5
                                                                                                                                     120.5
120.5
120.5
  123.5
123.5
123.5
123.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          071213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
    071213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOUTH TERMINATION OF THE SERVICE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \mathcal{S}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          071213 grapevine 1
039857 grapevine 1
08bep3 grapevine 2
096664 sugar beet
089910 sugar beet
00374 sugar beet
00374 sugar beet
00374 sugar beet
00379 cirus tris
09690 cirus tris
0990p0 cirus tris
0990p0 cirus tris
0990p2 cirus tris
                                                                                                                                                    7, 2003, 14:46:13; Search time 34 Seconds (without alignments) 1502.777 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                           991
1 MELMSDSNLSNLVITDASSL......GGVVNTPVSNLRQLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               stal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                      830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                summaries
                                                                                                                  using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  071213
089857
090629
096664
0089910
008531
008531
008585
099070
099070
099070
099070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                               BLCSJM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_bacteria:

sp_bacteria:

sp_fung:...

sp_human:...

sp_nammal:...

sp_mammal:...

sp_nammal:...

sp_nammal:...

sp_nammal:...

sp_nammal:...

sp_nammal:...

sp_nammal:...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ost-processing: Minimum Match 00% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inimum DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-613-486-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPTREMBL 23:*
                                                                                                                  protein search,
                                                                                                                                                              November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.9
30.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229.9
229.8
229.8
226.9
113.1
122.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erfect score:
                                                                                                                                                                                                                                                                                                                                                  coring table:
                                                                                                                    ı
                                                                                                                  W protein
                                                                                                                                                                                                                                                                                                      squence:
                                                                                                                                                                                                                                                                                                                                                                                                                   sarched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            itabase
                                                                                                                                                              0::
```

0

9 9

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=12161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BYV-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Closterovirus
                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62906D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
Q9Q6Z9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Q96664
                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                              \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOUNTERNAMENTAN SOUND SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 DFCIAYKHKLPQLNAAABLGIPAEDSYLAADFLGTCPKLSELQQSRKWFASNYALKTEGG 180
61 TISPKVQRADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Graperine leafroll-associated virus 2.
Viruses: ssNA positive-strand viruses, no DNA stago; Ciosteroviridae;
Closterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grapevine rootstock stem lesion associated virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
Closterovirus.
NCBI_TaxID=167634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TISPKVQRADSDVIFSNSFGERNVVVTGGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MELMSDSNLSNLVITDASSINGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALLARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Zhang Y., Rowhani A.;
"Nucleotide sequence of grapevine rootstock stem lesion associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abou-Gharem N.; "The nucleotide sequence of the 3'terminal region of grapevine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leafroll associated closterovirus 2.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; Y14131; CAN74566.1;
InterPro; IPR002679; Clost.
Pfam; PF01185; Closter coat.
SEQUENCE 198 AA; 21630 MW; 15D631E4088D3F01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF314061; AAN63472.1; -.
SEQUENCE 198 AA; 21620 MW; 370E95A9369734A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.3%; Score 984; DB 12; Best Local Similarity 99.5%; Pred. No. 3.7e-88; Matches 197; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                     198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                   181 VVNTPVSNLRQLGRREVM 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 VVNTPVSNLROLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 VVNTPVSNLROLGRREVM 198
                                                                                                        181 VVNTPVSNLRQLGRREVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=64003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8BEP3
                                                                                                                                                                                                                                                                  SULT 2
                                                                                                                                                                                                                                                                                                   9857
```

```
Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 SVQPTSTFIKASFGSGKELFLTHGELRSFLDSQKLLEGKPNKLRCFCRTFQKDYISFAKE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORADSDVIPSNSFGE-RNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIA 125
                                                                                                                                                                                                                      TISPKVORADSDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRIFGRIFTEAYV 120
                                                                                                                                                                                                                                                                                                                              DFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGG 180
                                                                                                                   ်
မ
                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 SNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ATFENVSLADQTC1HGEDCDKLRRDFEECLKLKGVPEDKLGLALG1CLYSCATIGTSNKV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                             1 MELMSDSNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAAR
                                                                                                                                                  1 MELMSDDNLSGLVITDASSLNGVDKKLLSAEVIKKLVQKGAPSQGIETVFGLLLYALAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of a plant virus.";
                                                           Gaps
                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cuery Match 30.0%; Score 297; DB 12; Length 204; Best Local Similarity 37.6%; Pred. No. 6.4e-21; Matches 71; Conservative 32; Mismatches 84; Indels 2
        Length 198;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peremyslov V.V., Hagiwara Y., Alzhanova D., Dolja V.V.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF190581; AF190581; AF1905851; Closter_coat. Pfam; PF01785; Closter_coat. SEQUENCE 204 AA; 22419 MW; FD6337E1D2490D33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9Q6Z9,
01-XAY-2000 (TrEMBLrel. 13, Created)
01-XAY-2000 (TrEMBLrel. 13, Last sequence update)
19-YAR-2003 (TrEMBLrel. 23, Last annotation update)
Major capsid protein.
Sugar beet yellow virus (SBYV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BYV-4;
MEDLINE=20079557; PubMed=10611288;
MEDLINE=20079557; PubMed=10611288;
V.V., Hagiwara Y., Dolja V.V.;
"HSP70 homolog functions in Cell-to-cell movement "HSP70 homolog functions in Cell-to-cell movement Proc. Natl. Acad. Sci. U.S.A. 96:14771-14776 (1999)
  92.9%; Score 921; DB 12; 90.9%; Pred. No. 5.4e-82; iive 10; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                      181 VVNTPVSNLRCLGRREVM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVNTPVSNIRCLGRREVM
Query Match
Best Local Similarity 90.99
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VISLKQLGR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSNLRQLGR 194
```

```
22446 MW; D913184ECC93883B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. C1, Created)
01-NOV-1996 (TrEMBLrel. C1, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                       |::|:|||
VTSLKQLGR 198
                                                                                                                                                                                                                                                                                                                    VSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 VSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Broom's barn;
     204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Z.)
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=12161;
                                                                                                                                                                                                                                                                                                                    186
   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          203724;
                                                                                                                                                                                                                                                                                                                                                                                                                                      203724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           D,
                                                                                                                                                                         ò
                                                                                                                                                                                                          S
                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVQPTSTFIKASFGSGKELFLTHGELRSFLDSQKILEGKPNKLRCFCRTFQKDYISFAXE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 QRADSDVIFSNSFGE-RNVVVTEGDLKKVIDGCAPLTRFTNKLRTFGRTFTEAYVDFCIA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 ATFENVSLVDQTCLHGEDCDKLRRNFEECLKLKGVPEDKLGLALGJCLYSCATIGTSNKV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Major coat protein.
Sugar beet yellow virus (SBYV).
Viruses; seRNA positive-strand viruses, no DNA stage; Closteroviridae;
Closterovirus.
VCBI_TAXID=12161;
                                                                     Coat protein (Fragment).
Sugar beet yellow virus (SBYV).
Viruses; sSRNA positive-strand viruses, no DNA stage; Closterovirus.
Closterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 SNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKV
                                                                                                                                                                                                                           Creamer R., He X.H., Yang C.H., Grantham G.; "Characterization of the 3'-proximal encoded proteins of beet yellows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 YKHKLPQLNAAAELGIPAEDSYLAADFIGTCPKISELQQSRKMFASMYALKTEGGVVNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRANS-CAlifornian;
MEDLINE-98285746; PubMed=9621048;
MEDLINE-98285746; Hagiwara Y., Dolja V.V.;
"Genes required for replication of the 15.5-kilobase RNA genome of plant closterovirus.";
"J Virol. 72:5870-5876 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.9%; Score 296; DB 12; Length 204; Best Local Similarity 37.6%; Pred. No. 8e-21; Matches 71; Conservative 32; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Californian;
Dolja V., Peremyslov V., Hagivara Y.;
Submitted (MAR.1998) to the EMBL/GenBank/DDBC databases.
EMBL, AFOS6575, AZC251201; -.
INTEPPC; IPR002679; Closter_coat.
Pfam: PF01785; Closter_coat.
Coat protein.
                                                                                                                                                                                                                                                             closterovirus.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                204 204 204 204 204 204 204 3A; D082C33ECC93883B CRC64;
                                01-FEB-1997 (TrEMEirel. C2, Created)
01-FEB-1997 (TrEMEirel. C2, Last sequence update)
01-MAR-2003 (TrEMBirel. 23, Last annotation update)
 204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                            EMBL, U71295; AAB17031.1; -.
InterPro, IPR002679; Closter_coat.
Pfam, PF01785; Closter_coat; 1.
                                                                                                                                                                                                          STRAIN=California BYV-CA;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 VSNLROLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 VTSLKOLGR 198
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID=12161;
                                                                                                                                                                                                                                                                                                                                                NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          089910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SULT 6
```

```
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                 67 ORADSDVIFSNSFGE-RNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIA 125
                                                                                                                                                                                                                                                                                                                                                                                                                    126 YKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQOSRKMPASMYALKTEGGVVNTP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 YKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGGVVNTP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 QRADSDVIFSNSF-GERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brunstedt J., Moseley J., Hull R.; "Nucleotide sequence of cDNA encoding the coat protein of beet yellows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugar beet yellow virus (SBYV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
Closterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 SVQPTSTFIKASFGGGKELFLTHGELRSFLDSQKLLEGKPNKLRCFCRTFQKDYISFAKE
                                                                                                                                          7 SNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKV
                                                                                                                                                                                      1 SVQPTSTFIKASFGSGKELFLTHGELRSFLDSQKLLEGKPNKLRCFCRTFQKDYISFAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 SNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKV
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=German,
Agranovsky A.A., Koonin E.Y., Boyko V.P., Maiss E., Lurina N.A.,
Agranovsky A.A., Koonin E.Y., Boyko V.P., Maiss E., Lurina N.A.,
Agranovsky J.G.,
Alabekov J.G.,
"Beet yellows closterovirus: complete genome structure and
identification of a leader papain-like thiol protease.";
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
EMBL, M59452; AAA722551; -.
EMBL, X73475; CAA51861.1; -.
EMBL, X73475; CAA51861.1; -.
InterPro: IPR002679; Closter coat.
Pfam; PF01785; Closter coat.
Pfam; PF01785; Closter coat.
SEQUENCE 204 AA; 22388 WW; 92B2A4DCA77543D9 CRC64;
                                                                        5;
Query Match 29.8%; Score 295; DB 12; Length 204; Best Local Similarity 37.6%; Pred. No. 1e-20; Matches 71; Conservative 31; Mismatches 85; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cuery Match 29.6%; Score 293; DB 12; Length 204; Best Local Similarity 37.6%; Pred. No. 1.6e-20; Matches 71; Conservative 31; Mismatches 85; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases
```

008531

```
90 KTPLVSAKIDAVNVIITYEDIKNFVNSLTLLKNYKNKIRVFARTFEEFYLRFVRCYKHIL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 SDVIFSNSFGERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIAYHHKL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 POLNAAAELGIPAEDSYLAAJFLGTCPKLSELQQSRKMFASMYALKTEGGVVNTPVSNLR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 MNLHIDPIL--IAMADVRQLGTQQNAALNRDL--FLTLKGKYPNLPDEDXDFHIAMMLYR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MELMSDSNLSNLVITDASSLNGVDKKLLSAEVEXMLVQKG----APNEGIEVVFGLLLYA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 LAARTIS--------PKVQRAD---SDVIF-SNSFGERNVVVTEGDLXKVJD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Citrus tristeza virus.
Viruses; seRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                           "Characterization of the beet yellow stunt virus coat protein gene.";
Phytopathology 88:1040-1045(1998).

BMBL; US1931; AACS565.1;
InterPro; IPR002679; Closter coat.
InterPro; IPR002048; EF-hand.
Pfam; PF01785; Closter coat;
InterPro; IPR00208; EF-hand.

Pfam; PF01785; Closter coat;
SEQUENCE 215 AA; Z3696 MM; 91185835840806FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 NIVITDASSLNGVDKKLLSAEVEKMLVQKGAPNEGIEVVFGLLLYALAARTTSPKVGRAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 NFARASATCLNGENKKKLFEEFSVRVKTQDVTESGIPTTLGMTLYALATLSTSSKIDIED
                                        SEQUENCE FROM N.A. MEDLINE-96266429; PubMed=8661428; MEDLINE-96266429; PubMed=8661428; Michaeva O.V., Mushegian A.R., Lee R.F., Dawson W.O. "Organization of the 3'-terminal half of beet yellow stunt virus genome and implications for the evolution of closteroviruses."; Virology 221:199-207(1996).
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Karasev A.V., Nikolaeva O.V., Lee R.F., Wisler G.C., Duffus J.E.
Dawson W.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.9%; Score 266.5; DB 12; Length 215; Best Local Similarity 36.1%; Pred. No. 6.7e-18; Matches 66; Conservative 22; Mismatches 94; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roy A., Ramachandran P., Brlansky R.H.;
"Molecular characterization of Indian Citrus tristeza virus
isolates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cuery Match.

13.2%; Score 130.5; DB 12; Length.

Best Local Similarity 27.7%; Pred. No. 0.00014;

Matches 61; Conservative 27; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2002) to the EMBL/GenBank/DDBC databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AF501867; AAM22216.1; -
InterPro; IPR002679; Closter coat.
Pfam; PF01785; Closter_coat; 1.
SEQUENCE 223 AA; 24903 MW; 9D31F82AD158B649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8JYV1;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=12162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 076 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 YLG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
                NARARKERKERKOOOOOOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SON SET TAPEN OCCOSSION OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Op.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 QRADSDVIFSNSF-GERNVVVTEGDLKKVLDGCAPLTRFTNKLRTFGRTFTEAYVDFCIA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 NVQPTSTFIKASFGGGKELY1THGELNSFLGSQKLLEGKPNKLRCFCRTFQKDYISLRKE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 ATPENVSLADQTCLHGEDCDKLRKNFEECLKLKGVPEDNLGIALGLCLYSCATIGTSNKV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 SNLSNLVITDASSLNGVDKKLLSAEVEKMLVOKGAPNEGIEVVFGLLLYALAARTISPKV 66
                                                                                                                                                                                                                                 Q0B531;
O1-NOV-1996 (TrEMBLrel. CI, Created)
01-NOV-1996 (TrEMBLrel. OI), Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Coat protein.
Coat protein.
Sugar beet yellow virus (SBVV).
Viruses; sSRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      065858;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Coat protein.
Beet yellow stunt virus.
Niruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
Closterovirus.
NCBI_TAXID=35290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 YRHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRKMFASMYALKTEGGVVNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dolja V.V.; "Nucleotide sequence of the 3'-terminal half of beet yellows closterovirus RNA genome: unique arrangement of eight virus genes."; J. Gen. Virol. 72:15-23(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=91116305; PubMed=1990061;
Agranovsky A.A., Boyko V.P., Karasev A.V., Lunina N.A., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.9%; Score 286; DB 12; Length 204; 37.6%; Pred. No. 7.7e-20; tive 29; Mismatches 87; Indels 5
                                                                                                                                                                                                          204 AA
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-UKRAINIAN;
MEDLINE-94082464; PubMed-8259666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 37.6
Matches 71; Conservative
                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
|::|:|:|
190 VTSLKQLGR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |::|:||:||
190 VTSLKQLGR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 VSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Closterovirus.
NCBI_TaxID=1216:;
```

Query Match

11;

57; Gaps

065858

-1

٦,

```
64 -------PKVQRAD---SDVIF-SNSFGERNVVVTEGDLKKVLDGCAPLTRFTNK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 LRIFGRIFIEAYVDFCIAYKHKLPQJNAAAELGIPAEDSYJAADFLGTCPKLSELQQSRK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 LRVWGRTNDALYLAFC-RQNRNLSYGGRPLDAGIPAGYHYLCADFL-TGAGLTDLECAVY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 LDGCAPLTRFTNKLRTFGRTFTEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 IAMNDVRQLGTQQNAALNRDL--FLTLKGKYPNLPDKDKDFHLAMMLYRLAVKSSSLQSD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 LAARTISPKVORAD------SOLIF-SNSFGERNVVVTEGDLKKV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MELMSDSNLSNLVITDASSLNGVDKKLLSAEVEKMLVQKG----APNEGIEVVFGLLLYA 56
   no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 LVITDASSLNGVDKKLLSAEVEKMIVQKG----APNEGIEVVFGLILYALAARTTS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 DDTTGVTYTRDGVEVELSDKLWTDVVPNSKGIGNR------TNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 MNLHIDPTL--IAMNOVROLGTOONAALNRDL--FLTLKGKYPNLPDKDKDFHIAMMLYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEATURETANTI;
STRAIN=TANTI;
STRAIN=TANTI;
STRAIN=TANTI;
STRAIN=TANTI;
STRAIN=TANTI;
Martinez-Soriano J.P.;
Martinez-Soriano J.P.;
Molecular Analysis of Citrus tristeza virus from Mexico.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF342890; AAK27476.1;
InterPro; IPR002679; Closter_coat.
InterPro; IPR002679; Closter_coat.
Pfam; PF01785; Closter_coat.
SEQUENCE 223 AA; 24868 MW; 6EA0C742D2212949 CRC64;
                                                                                                                                                                                         Partinez.-15. July Villarreal-Garcia J.A., Rivera-Bustamante Martinez-Soriano J.P.;
Martinez-Soriano J.P.;
Molecular Analysis of Citrus tristeza virus from Mexico.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF342894; AAK27480.1;
InterPro; IPR002679; Closter coat.
Pfam; PF0.785; Closter coat.
SEQUENCE 222 AA; 24741 MW; SBFA27BCB4B08DDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 LAVKSSS--LOSDDDTTGITYTREGVDVDLPDKLWTDVVFNSKGIGNR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
12.7%; Score 125.5; DB 12; Length
Best Local Similarity 26.8%; Pred. No. 0.00044;
Matches 56; Conservative 29; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update;
Last annotation update;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.7%; Score 125.5; DB 12; Best Local Similarity 27.0%; Pred. No. 0.00044; Matches 60; Conservative 27; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 MFASMYALKTEGG -- VVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Citrus tristeza virus.
Viruses, ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Closterovirus.
NCBI_TaxID=12162;
                                                                       NCBI_TaxID=12162;
                                                                                                                                                                          STRAIN=BC15-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
   SOURTH PARK NOCCOSE THE POUR SOUR THE PARK NOCCOSE THE PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------PKVQRAD---SDVIF-SNSFGERNVVVTEGDIKKVIDGCAPLIRFINK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 DDTTGITYTREGVEVDLSDKLWTDIVYNSKCIGNR------TNA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 LRTFGRIFTEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPKLSELQQSRX 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 GCAPLTRFTNKLRTFGRTFTEAYVDFGIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTC 156
                                                                                                                                                                133 -----TNALKVWGRTNDALYLAFC-RONRNLSYGGRPLDAGIPAGYHYLCADFL-TG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=25-20;
Sequeira-Z., Nolasco G.;
"Bacterial expressed coat protein for the development of a single
antibody for routine detection of Cirrus Tristeza Virus in Portugal.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 ITMNDVRQLSTQQNAALNRD1--FLALKGKYPNLPDKDKDFHIAMMLYRLAVKSSSLQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Citrus tristeza virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Ciosteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonacalza B., Febres V., Niblett C.L., Nolasco G.; "Biomolecular characterization of Citrus Tristeza Virus isolates from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 LVITDASSLNGVDKKLLSAEVEKMLVQKG----APNEGIEVVFGLLLYALAARTTS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12; Length 223;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases EMBL, AF184115; AAD56568.1; -..
InterPro: 1PR002679; Closter_coat.
Pfam; PF01785; Closter_coat.; 1.
SEQUENCE 223 AA; 24930 MW; 05C4D6BD17C2D7F0 CRC64;
                                                                                                                                                                                                                                   157 PKLSELOQSRKMFASMYALKTEGG--VVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.1%; Score 129.5; DB 12; Best Local Similarity 26.3%; Pred. No. 0.00018; Matches 55; Conservative 31; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 MFASMYALKTEGG -- VVNTPVSNIRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 IQAKEQLLKKRGGDEVV---VTNVRQLGK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created: 01-MAY-2000 (TrEMBLrel. 13, Last seq 01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0990P0;
01-JUN-2001 (TrEMBLrel. 17, Cr
01-JUN-2001 (TrEMBLrel. 17, La
01-OCT-2001 (TrEMBLrel. 18, La
Coat protein.
Citrus tristeza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Closterovirus.
NCBI_TaxID=12162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Portugal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9QEG4
Q9QEG4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         040660
                                                                                                                                                                                                                                                                                                                                                                                                       ESULT 11
```

```
Coat protein
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search cor
Job time
    ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 LDGCAPLTRFTNKLRTFGRTFTEAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLG 154
-----TNALRVWGRTNDALYLAFC-RQNRNLSYGGRPLDAGIPAGYHYLCADFL- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MELMSDSNLSNLV1TDASSLNGVDKKLLSAEVEKMLVQKG----APNEGIEVVFGLLLYA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 LAARITSPKVQRAD------SDVIF-SNSFGERNVVVTEGDLKKV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 MNLHIDPTL--IAMNDVRQLGTCQNAALNRDL--FLTLKGKHPNLPDKDKDFHIAMKLYR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE ...

STRAIN=19-21;
Sequeira 2., Nolasco G.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, AF184141, AADS6567.1;
Interpro; IPR02679; Closter coat.
Interpro; IPR02679; Closter coat.
SEQUENCE 223 AA; 24ā86 MW; 20723BA19E2CBFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Charton coat protein.
Citrus tristeza virus (isolate T36) (CTV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                Coat protein.
Citrus tristeza virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 LAVKSSS--IQSEDETTGITYTREGVEVELPDKLWTDVVFNSKGIGNR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonacalza B., Febres V., Niblett C.L., Nolasco G.; *Biomolecular characterization of Citrus Tristeza Virus isolates from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 27.0%; Pred. No. 0.00044;
Matches 60; Conservative 27; Mismatches 74; Indels 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 TCPKLSELQQSRKMFASMYALKTEGG--VVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAGLTDLECAVYIQAKEQLLKKRGADEVV---VINVRQLGK 219
                                                                                        155 TCPKLSELQQSRKMFASMYALKTEGG--VVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT:
                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                     Q9QEG5;
01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=12162;
                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Closterovirus.
NCBI_TaxID=31712;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM STRAIN=19-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8B3T3;
Q8B3T3;
                                                                                                                                                                       SULT 14
```

```
133 -----TNALRVWGRTNDALYLARC-RQNRNLSYGGRPLDAGIPAGYHYLCADFL-TGAG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
MEDLINE=99307427; PubMed=10377432; Satyanarayana T. Gowda S., Boykc V.P., Albiach-Marti M.R., Satyanarayana T., Gowda S., Boykc V.P., Albiach-Marti M.B., Mawassi M., Navas-Castillo J., Karasev A.V., Dolja V., Hilf M.B., Lewandowski D.J., Moreno P., Bar-Joseph M., Garnsey S.M., Dawson W.O., "An engineered closterovirus RNA replicon and analysis of heterologous terminal sequences for replication."

Lerminal sequences for replication."

Proc. Natl. Acad. Sci. U.S.A. 96:7433-7438(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------PNEGIEVVFGLLLYALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 SSVNLHIDPTLITMNDVRQLSTQQNAAINRDLFLTLKGKGFNLPDKDKDFHIAMMLYRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 ARTTS-------PKVQRAD---SDVIF-SNSFGERNVVTEGDLKKVLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 APLTRFTNKURTFGRTFTBAYVDFCIAYKHKLPQLNAAAELGIPAEDSYLAADFLGTCPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 59
                                                                                                                                                                                                                                                                                                                           Satyanarayana T., Gowda S., Ayilon W.A., Dawson W.C., "Frameshift mutations in infectious cDNA clones of Citrus tris virus: A strategy to minimize the toxicity of viral sequences Escherichia coli."; Submitted (OCT-2002) to the EMBL/GenBark/DDBJ databases.
EMBL, AYICG68, AAO12723.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.6%; Score 125; DB 12; Length 223; 25.9%; Pred. No. 0.00049; cive 13; Mismatches 63; Indels 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 VKSSSLQSDDDATGITYTREGVEVDLSDKLWTDVVFNSKGIGNR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 AA; 24890 MW; 5132F5E753023061 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTDLECAVYIQAKEQLLK-KRGADDVVVTNVRQLGK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 LSELQQSRKMFASMYALKTEGGVVNTPVSNLRQLGR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 SSLN-GVDKKLLSA-EVEKMLVQKGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              completed: November 7, 2003, 14:49:49
ne : 36 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.9%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
```

29: gb_gss2:*

Н

```
QGFION21.yg.abl QC EFGHJ lettuce serriola Lactuca sativa cDNA clone QGFION21, mRNA sequence.
BQ986943
BQ986943.1 GI:22404468
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactuca sativa
bakaryota, Vizidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                BG247808
BH096256
BU343622
BJ435395
                                                                                                                                                                                                                                                                                                                                                                               C92123
CB343251
BG421690
                                                                                                                                                                                                                                                                                                                                                                                                                  AQ949879
CB569015
BI773596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG544734
CC155340
AZ079289
                                                                                                                                                                                                                                                BQ984758
BG526441
BG523153
                                                                                                                   BQ986943
BZ051926
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BU026578
BQ481813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA582924
BU202935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH929686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI085103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ969618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ691220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI199349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ951071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA316784
                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                     627
750
828
923
1028
428
560
606
513
727
836
432
                                                                                 Query
Match Length
                                                                                                                                                                                                                                                                                                                      732
                                                                                                                                                                                                                                                                                                                                                                   644
704
600
                                                                                                                                                                                                                                                                                                                                                                                                                             762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactuca sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.5
81.5
81.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.5
83
                                                                                                                                                                                                                                     83.5
83.5
83.5
                                                                                             Score
                                                                                                                                                     83.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
BQ986943
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O
                                                                                                                                                                               υo
                                                                                                                                                                                                                                                                                                                                                                nmand line parameters:
(CDSL=frame+_p2n.model -DEV-x1h)
(CDSL=frame+_p2n.model -DEV-x1h)
)=/cgn2_1/USPTO_spool/USC961486/Funat_07112603_120411_27105/app_query.fasta_1.391
)=/cgn2_1/USPTO_spool/USC961486/Funat_0712603_1_EOOOCH=6_-LOOOPEXT=0
)B-EST -OPMT-fastap -SUDE1X-stst -MINMATCH=0.1 -EOOCCH=6_-LOOOPEXT=0
)MITS=bits -START=1 -EXDE=-1 -MATRIX=blosum62 -TRANS=human43.cdi -LIST=45
)MCALIGN=200 -THR SCORE=pcr -THR MAX=100 -THR MINE 0 -ALIGN=15 -NODE=LCCAL
UTFMT-pcc -NORM=ext -HRAPSIZE=550 -MINLEN=0 -MAXLEN=2000000000
SER=USG9613486 @CSN : 1_281.0 @xunat_07112093_120411_27105 -NOPU=6_-ICPU=3
OFMAPP_LARGEQUERSY -NGE_SCOREE_SC -WAIT -DSPEDGOK=100_-LONGLOG
EV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPOXT=0.5 -FGAPOP=6
GAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                  November 7, 2003, 20:42:48; Search time 2044 Seconds (without alignments) 2354.347 Million cell updates/sec
                                                                                                                               991
1 MELMSDSNLSNLVITDASSL......GGVVNTPVSNLRQLGRREVM 198
                                                                                                                                                                                                                                                             45562784
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                              - nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                     22781392 segs, 12152238056 residues
                                                                                                                                                                                                                                                             otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                             2.00.7
                                                                                                                                                         BLOSUM62
Xgapop 10.C , Xgapext
Ygapop 10.C , Ygapext
Fgapop 6.0 , Fgapext
Pelop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gss hum:*
gss inv:*
gss pln:*
                                                                                                                                                                                                                                                                                   seg length: 0
seg length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_est3:*
gb_est4:*
gb_est5:*
em_estfun:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gss_pro:*
gss_rod:*
gss_phg:*
gss_vrl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gss_vrt:
gss_fun:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .snm_ssg_
                                                                                                                   US-09-613-486-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          em_estban.
em_esthum..
em_estin...
em_estin...
em_estpl...
em_estpl...
em_estpl...
em_estpl...
em_estpl...
em_estpl...
em_estpl...
em_estpl...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gss mam:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_estcm:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ē,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ę,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESI:*
                                                                                                                   itle:
erfect score:
                                                                                                                                                                  coring table:
                                                                                                                                                                                                                                                                                   inimum DB
                                               M protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tabase :
                                                                                                                                           equence:
                                                                                                                                                                                                                                      earched:
                                                                       un on:
```

603102659 E2700 Chi CSU-K34.1 SPCI-23-4 Sheared D odh9aced D odh9aced Sheared D odb9aced D

BG544734 | CC155340 | AZ079289 | AQ951071 BH929686

BQ481813 PV GEa012 BU410316 603158538

EST002599

CA582924 BU202935

CA316784 UI-M-FWC-AZ691220 ENTJJ41TF BI199349 602759615

CHB39B11

BI085103 BU765335 BQ969618

BZ577160

82051926 JRIESTRAD BAN32003 TRESTRAD BAN32003 TRESTRAD BAN33095 HAA08017 BUOC7723 QGHSE15.Y BAN33495 BA133495 BA376355 BA137635 BA376355 BA376355 BA376355 BA376355 BA376355 BA376355 BA97636 QGA7M01.Y BC98416 GQA7M01.Y BC98416 GQA7M01.Y BC526441 61-95 Ete BC523141 61-95 Ete BC523141 61-95 Ete BC523141 61-95 Ete BC93104 QGA77F14. BC993104 QGA77F14. BC98218 QGA67F01. BC98218 QGA67F01. BC993104 QGA77F14. BC98218 QGA67F01. BC993104 QGA77F14. BC993104 QGA77F14. BC993104 QGA77F17. BC993104 AGBVCCURT. BC99919 SPGARTED AGBVCCURT. BC99919 AGBVCCURT. BC777596 FC31173.Y

us-09-613-486-15.rst

COURNAL

TITLE MMENT TATURES

```
core eudicots; rosids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BZC51926 1748 bp DNA linear GSS 09-OCT-2002
jnr57h07.g1 B.oleracea001 Brassica oleracea genomic, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica oleracea
Exassica oleracea
Eukaryota, Olirdiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
'eurosids II; Brassicales; Brassicaceae; Brassica.
1 (Dases 1 to 748)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, Whole genome shotgun reads from Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="B.oleracea001"
/note="Vector: p07041; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica cleracea T01000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Babinowicz (CSH1) and the shotgun library prepared at Washington University Genome
                                                                                                                        -----ThrPheGlyArg---ThrPheThrGluAlaTyrValAspPheCysIleAlaTyr 126
                                                                                                                                                                                                                                                                                                                                                                                                   365 AAGGTGGATTCTTTGGTCCCACTTGCGGAAATGTTTCAGTATGTGGAGTACTTTAAGG
                                                                                                                                                                                                                                                                                    --TyrreuAla-----AlaAspPhereuGlyThrCysPro
      ----ArgPheThrAsnLysLeuArg
                                                                                                                                                                           425 GGAATGACAAAAGGGAGAGCTTCTTACACAATGCAATTAGCTAAATTTGATGTTGTGCCT
                                                                                                                                                                                                                                       127 LysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               748
333
14
14
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: jnr57 row: h column: 07
Seq primer: -28RFPOT reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 LysleuSerGluleuGlnGlnSerArgLysMet 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATAGGAAAAAAAAAACAAAAACAAAGGATT 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
   LysValLeuAspGlyCysAlaProLeuThr----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence start: 56
High quality sequence stop: 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-613-486-15 (1-198) x BZ051926 (1-748)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing Center."
164 c 136 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BZ051926
BZ051926.1 GI:23652910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.96
88.50
47.00%
33.00%
8.93%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: shotgur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               605
                                                                                                                        110
      93
                                                                                                                                                                                                                                                                                                                                                                147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
CRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
CRSANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BZ051926/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                     감
                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                          Q:
                                                                                                                                                                                                                                                                                                                                                       ें
                                                                                                                                                                                                                                                                                                                                                                                                                      D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                      90
                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /alone_lib="QEFGHJ lettuce serriola"
/alone_lib="QEFGHJ lettuce serriola"
/alone="Vector: pBRcDNA£iAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=GE_EGFMinating seeds
TAG_LIB=GE_EGFMinating seeds
Cichorieae; Lactuca,
I (bases I to 706)

Kozik, A., Wichelmore, R.W., Knapp, S., Marvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Zlegle, C., Ellison,
L.P., Kolfwan, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Zackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://comggenomics.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 GTTGAAGTTGTGACGCCTGAAGACATTTGGGGGATGTGGATTTGGAATTCGAGA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 GTTTTGACCGAT---GGGTCCTACCATGATGTTGACTCCAGTGTCCTTGCGTTCCAG--- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                       Contacts. Alexander Kozik (R. W. Michelmore)
Department of Vegetable Crops, R. W. Michelmore Lab
Department of Vegetable Crops, R. W. Michelmore Lab
Department of Vegetable Crops, R. W. Michelmore Lab
Diversity of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1 (530)-752-9659
Fax: 1-(530)-752-9659
Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 ------AsnSerPheGlyGluArgAsnValValValThrGluGlyAspLeuLys 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 VallleThrAspAlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGluVal 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 LeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLys-------ValGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 GluiysMetLeuValGlniysGlyAlaProAsnGluGlyIleGluValValPheGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 -----Ciggcagcacacagagagacatricagaaagaigir--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               706
51
28
53
59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Corservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Lactuca sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
cultivar="i.serriola"
/db_xref="taxon:4236"
/clone="QGF(0N21"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-613-486-15 (1-198) x BQ986943 (1-706)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_SEQ=TCTGTGCGGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.882
68.50
41.36%
26.70%
8.93%
                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               st Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rcent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ignment Scores:
ed. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SE COUNT
IGIN
                                         JFERENCE
AUTHORS
```

```
Hordeum vulgare subsp. vulgare
Lordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
The subtracted library was electroporated into DH10B (GeneHog, Invitrogen, Inc). WARNING: the library contains a small percentage of cDNAs derived from the human host cells. Library Scource: David Sibley, Washington University."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 Trerecaesaceaecarrarrarrarrarraraeaarracaerraeaegeserrerraraaaaa 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 LysieuProGlnLeuAsnAlaAla --- AlaGluLeuGlyIleProAlaGluAspSerTyr 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluGlyAspLeuLysLys---ValLeuAspGlyCysAlaProLeuThrArgPheThrAsn 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 GAGGGGAGGTTGGGCAGCATAGTTCTCTTCGACTGTGTCCCCCCCTTTGAGGTACACGAAC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PheGlyArgThr 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 PheThrGluAlaTyrValAspPheCysIle--------------AlaTyrLysHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 GAAGACAGGAGTGCGGGATACAACATTTCTCCTTTTCCAGTCTTCATGCTTTTCAGGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA linear EST 30-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Research (IPK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potokina, E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 LeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGlu 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 CAGAGTACATCGACATCGCGCAAATGTCCGGGCATCAGTGAA 421
                                                                                                                                                                                                                                                                               4477
111
20
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant F
Corrensstr. 3, 06466, Gatersleben, Germany
                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       00
                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562 bp
HA08017r HA Hordeum vulgare subsp.
5-PRIME, mRNA sequence.
EQ459495.
EQ459495.1 GI:21267266
                                                                                                                                                             124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticeae, Hordeum.
1 (bases 1 to 562)
Radchuk, V., Zhang, H., Weschke, W.,
Barley ESTs from developing seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="embryosac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:112509"
/clone="HA08017"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: stein@ipk-gatersleben.de
Insert Length: 562 Std Error:
Plate: 8 row: O column: 17
Seg primer: M13rev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-613-486-15 (1-198) x BM132093 (1-477)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysbeuArgThr------
                                                                                                                                                             114 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Stein Nils
                                                                                                                                                             121 c
                                                                                                                                                                                                                                                                               0.776
87.00
43.62%
31.91%
8.78%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corrensstr. 3, 06
Tel: 039482-5522
Fax: 039482-5595
                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                         Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSICN
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LCCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                         Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
BQ459495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \dot{\varsigma}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / organism="roxoplasma gondil"
/ organism="roxoplasma gondil"
/ strain="RH (Type 1)"
/ clone="TgEST2yb06607.yl"
/ clone="TgEST2yb06607.yl"
/ dev_stage="Tachyzoite"
/ dev_stage="Tachyzoite"
/ dev_stage="Tachyzoite"
/ dev_stage="TgEST2yb06607.yl"
/ dev_stage="TgEST2yb06607.yl"
/ dev_stage="TgEST2yb06607.yl"
/ dev_stage="TgEST2yb06607.yl"
/ dev_stage="TgEST2yb06607.yl"
/ dev_stage="TgEH Tachyzoite"
/ dev_stage="TgEH"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM132093 477 bp mRNA linear EST 27-NOV-2001
TgESTzyb06e07.y1 TgRH Tachyzoite Subtracted cDNA Library Toxoplasma
gondii cDNA clone TgESTzyb06e07.y1 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                du) for further
or clone availability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Cole, R., Martin, J., Wylie, T., Dante, M., Marta, M., Martin, J., Wylie, T., Dante, M., Marta, M., Marter, M., Martan, M., Miller, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R., Toxoplasma EST Project
                                                                  551 ATAACCATCGTGGAAGGCACCTACGACAAATCTTAGGGAGTGATGGCCTGACGATGCTC 492
                                                                                                                                                                                                                                                                                                           TTTGATCTCAAGGAGGAGGTCACAAGATTACAGGGTTCCATGGACGAGCTGGCGCGCGACT 372
                                                                                                                                                                                                                                                                                                                                                                           141 IleProAlaGluAspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 CCTGCACAACCAACCAAGAAG-------CTAGAAGCTAAGACTGGT 282
                                                                                                                              ThrargPheThrashlysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAsp 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 GlubeuglingInSerArguysMetPheAlaSerMetTyrAlaLeubysThrGlugiyGly 180
         ValValValThrGluGlyAspLeuLysLysValLeu----AspGlyCysAlaProLeu 131
                                                                                                                                                                                                                                                   122 PheCysIleAlaTyrLys---HisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                             Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MC 63108, USA
Tal: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toxoplasma gondii
Toxoplasma gondii
Toxoplasma gondii
Bukaryota, Alvedata, Apicomplexa, Coccidia, Eimeriida,
Barcocystidae, Toxoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: toxo@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu)
information relating to organism, libraries, or
Seq primer: -40RP from Gibco
High quality sequence stop: 420.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Toxoplasma gondii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EM132093.1 GI:17126645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Clifton, S.
                                                                                                                                 102
                                                                                                                                                                                                                                                                                                               431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CESSION
RSION
YWORDS
URCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUS
FINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
MMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SULT 3
132093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATURES
```

```
Lactuca sativa

Lactuca sativa

Lactuca sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
spermatophyta; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.

E (bases 1 to 660)

E (cichorieae; Lactuca.

Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison,P., Kolkman,J., Slabaudh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower Eors from the Compositae Genome Project

http://compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Mol type="MRNA"

/ cultivar="L.serticla"

/ cultivar="L.serticla"

/ cultivar="L.serticla"

/ clone="GGHSEIS"

/ clone="GGHSEIS"

/ clone="GGHSEIS"

/ clone="VGCCOT: PBRCDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5° and 3' tags for distinguish each source of RNA. Chons were then pooled, size-fracticnated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LISUG_EFCHJ lettuce serriola

TAG_LISUG_EFCHJ lettuce serriola

TAG_LISUG=chemical induction

TAG_SEQ=CHAGGCGGG"

10 thers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --------AGGAAAGCTGCTCCAAAGATCTTGGAGCCGATATGAGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
Noiversity of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Emai: 1-(530)-752-9659
Emai: akozik@atgc.org [michelmore@vegmaii.ucdavis.edu]
belorgs to contig QG_CA_Contig3108, see http://cgpdb.ucdavis.edu/
for details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 ValileThrAspAlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 GluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPheGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 AlaAsp---------SerAspValllePheSer------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CTGCAGCACGAGGGCGTTTCGGGAAGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLys-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Lactuca sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: QGHS row: E column: 15.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-613-486-15 (1-198) x BU007723 (1-666)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.98
85.50
40.78%
27.93%
8.63%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
CRIGIN
           SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                      TILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω̈́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                               /done libe "HA"
//done 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G66 bp mRNA linear EST 22-AUG-2002 QGHSE15.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone QGHSE15, mRNA sequence.
BU007723.
BU007723.1 G1:22442118
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397 CCTGACGAATACACTTATGTCTTA-----CTCATTGAGTCCTGCTTCAGGTTGATAAT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 CTTGGGAGGAACGGGAGGTTAGATGATGATGGAGTTGTTTGATAGGATGTGCAAAGAG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 CATGACCCTCCCÁGAGGATTGCTGTGAATCTTGGTAGTTTTAATGTGATGGTTGATGCT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 CysAlaProLeuThrArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGiu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 TACTGCGGTGTGGAAAGGTTCCAGGATGCAATTGAGGTGTTTGGCAAAATGGGTGAGAAG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LysHisLys 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 LeuProGinLeuAsnAlaAlaAlaGluLeu-----141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 CTT-----GTTGGTGAGGCAGAAGAATTGTACAAGGAGATGGGGGAGCGTGGTATTAAT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 ProAlaGluAspSerTyrLeuAlaAspPheLeuGlyThrCysProLysLeuSerGlu 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 LeuGinGinSerArgLysMetPheAlaSerMetTyr-----AlaLeuLysThrGluGly 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451 GIGGAIGACGCIGITGGITACTICAGCAAGAIGITIGATGITGGICTCAGGCCCAATGCC 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 ProAsnGluGly1leGluValValPheGlyLeuLeuTyrAlaLeuAlaAlaArgThr 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 ThrSerProLysValGlnArgAlaAspSerAspValIlePheSerAsnSerPheGlyGlu 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 ------ArgAsnValValValThrGluGlyAspLeuLysLysValLeuAspGly 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 GlyValAspLysLysLeuLeuSerAlaGluValGluLysMetLeuValGlnLysGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 ---GGAGAGGATCCAAGGTGAGATTTGGGGCTGTTAGCTACAACATGGTGCTTGATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="0-7 DAP (days after pollination)"
/lab_host="xL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyValValAsnThrProValSerAsnLeuArgGlnLeuGlyArg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511 AATGCCTTTAACAAAGTCATAAGTGGCTTGGTGAAGGTTGATAGG 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 552
33
33
84
88
84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 AlaTyrValAspPheCysIleAlaTyr-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -09-613-486-15 (1-198) x BQ459495 (1-562)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.54
85.50
40.00%
20.51%
8.63%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rcent Similarity:
st Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                        æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ignment Scores:
```

ery Match:

ed. No.:

ore:

SE COUNT

IGIN

310 GTTGAAGTTGTGACGCCTGAAGAATTTGGGGGATGTGAITGGGGATTTGAATTCGAGA 369

g

CUS FINITION

007723

SULT

CESSION RSION YWORDS

Oy 121ePheSerAsnSerPheGlyGluArgAsnValValThACluGlyAspLeuLys 92 73 ValilePheSerAsnSerPheGlyGluArgAsnValValThrGluGlyAspLeuLys 92 75 Till	Db 333GAAGGTGGTGAACCTAACAACATTATGTCAATGGCAACTATTAAC 277 Oy 149 AlaalaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGinSerArgLysMet 168	B244:64/c ECCUS.	Email: cdtown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq primer: FF Class: sheared ends. Location/Qualifiers Anol_type="genomic DNA" Anol_type="genomic DNA" Ab_xref="taxon:3712" Ab_xref="taxon:3712" Abone="BorRR91" Aclone="BorRR91" Aclone="BorRR91" Aclone="bhoSl; Site 1: BstXI; 1.6-2 kb sheared Anote="Vector: PhOSI; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into phOSI using BstXI linkers" OR:GIN
77	433495 bictyostelium discoideum cDNA library, VF Dictyostescoideum cDNA clone ddv22f05 3', mRNA sequence. 433495. GI:19408217 433495.1 GI:19408217 421405telium discoideum 42140611	Stage Unpublished MMENT Contact: Tadasu Shin-i National Institute of Genetics Iiil Yata, Mishaa, Shizuoka 411-8540, Japan Tal: 81-55-81-6856 Fax: 81-559-81-6856 Fax: 81-559-81-6856 Fax: 1-559-81-6856 Fax: 1-559-81-6856 Fax: 1-570-1-6866-8	ignment Scores:

ore:

ę

```
541 TIAGITIATGITGGIACTAATCATGIC 567
                                                                                                                                                                                                                                                                                                                                                                                      2.19
85.50
35.45%
24.34%
8.63%
                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
DNA Res.
99156227
10048482
                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                         Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                         SASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                         No.
                                                                                                                                                                                                                                                                                                                                                                         Alignment
Pred. No.:
JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                     FEATURES
                                            COMMENT
                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΩĢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \mathcal{S}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AU034876
AU034876 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dictyostelium discoideum.
Dictyostelium discoideum.
Dictyostelium discoideum.
Eukaryota; Mycetozca; Dictyosteliida; Dictyostelium.
Eukaryota; Mycetozca; Dictyosteliida; Dictyostelium.
Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                        455
                                                                                                                                                                                                                                                                                                                         419
                                                                                                                                                                                                                                                                                                                                                                                      380
                                                                                                                                                                                                                                                                                                                                                                                                                                                 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 AspSerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGln 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThr 184
                                                                                                                                                                                                                                                                                          53
                                                                                                                                                                                                                                                                                                                                                       72
                                                                                                                                                                     26
                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                ---LeuSerAlaGluValGlu 33
                                                                                                                                                                  7 SerAsnLeuSerAsnLeuVallleThrAspAlaSerSerLeuAsnGlyValAspLysLys
                                                                                                                                                                                                                                                       514 TITGCTTCTATGCCTTCATCCTCCAAGCAGCCAATGGGGGTCTCTACCAGGGAAATCAGAA
                                                                                                                                                                                                                                                                                                                                                    54 LeuTyrAlaLeuAlaAlaArgThrThrSerProLysValGlnArgAlaAspSerAsp---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 ThrasnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPheCysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 AlaTyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGlu
                                                                                                                                                                                                                                                                                       34 LysMetLeuValGlnLysGlyAlaProAsnGluGlylleGluValValPheGlyLeuleu
                                                                                                                                                                                                                                                                                                                       -----AACCCCAAGGÁGTCTTSCAATSTTGTCTTCTCC-----
                                                                                                                                                                                                                                                                                                                                                                                 418 ---------ACTACTTCTCCAGAGATTGAGTTGAGTCATGACAAA
                                                                                                                                                                                                                                                                                                                                                                                                            73 ------ArgAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                            379 GAGGAGGATGAGATTGAAAGACTGGTATTTGGAACTGAGTTTGGGGAAGTTGAGACATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValValThrGluG.yAspleuLysLysValleuAspGlyCysAlaProLeuThrArgPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 GATAAGCTCCTTTTCCCCCAAAGAGTTCTCACCAAAGCTCAGACGAAGGTGCTCTCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 TTCAGGAAAGATCTTAGTGATGTT---------GGGGTCAGGCTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 GIIGIGGCCACAGCIGAAGCACAGAIIGIGAIGGAC---GCIGCAAGGAAGGIIGAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 ACAAATCTGCAAAGAGCTGAGCACAAA-----GCTGAGAAACAASTTGAGAAGAGCT
                            407
499
300
81
47
8
                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                        Gaps:
                                                                                                                                     -09-613-486-15 (1-198) x BZ434184 (1-704)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 ProValSerAsnLeuArgGln 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAATCTCGAGTATGCGTGAA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU034876.1 GI:3800300
                           2.15
85.50
38.16%
23.67%
8.63%
                                                                                                                                                                                                                                                                                                                       154 AAG-----
                                                         rcent Similarity:
st Local Similarity:
                                                                                                                                                                                                                             27 Leu----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AU034876
                ignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165
                                                                                      ery Match:
                              .. ON .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CESSION
RSION
YWORDS
URCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SULT 8
034876
```

TITLE

CCS

```
104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATCATCATTGATTGCAGGTCATATGACA------CAATTAACAAGTGAAGAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 GluAlaTyrValAspPheCysIleAlaTyrLysHisLysLeuProGlnLeuAsnAlaAla 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaklaAspPheleuGlyThrCysProLysLeuSerGluLeuGlnGlnSerArgLysMet 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGCAGATTTCATCGCTGTCAAAGTTTCAAGTCATCCAGTCTATGATCCAATCTCTCAT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGAGGITAAGGITAGTGGTAAGAGACCAATTGAGAGATTGAGAGATTTGGGAGTATTA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       discoideum SL (H.Urushihara)"
t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPheGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysValGinArgAlaAspSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValllePheSerAsnSerPheGiyGluArgAsnValValValThrGluGiyAspLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::: |||| :::|||| TTGGGTGTTAAAGGTGTAAAACGTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ThrAsnLysLeuArgThrPheGlyArgThrPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 GCAGCTTACATTGATAAACTCTTGCAAATACTCATTCAATT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---GAAGGTGGTGAACCTGTAACACCATCATATAAGATTTTGTCAATGGCAACTATTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrProValSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysValLeuAspGlyCysAlaProLeuThrArgPhe----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427 GGTSCAAAGGCATTGGTATCGATGATAAAGTTGGTTCACTTCAAATTGGTAAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTGGTACTGATTCTGCCGCTAGTAATGATGATTTAGATATGTTGGGTGAATTACGTACT
                                                                                                                       1-1-1 Tennoudal Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
                                                                                                                                                                                                                                                                                                                                 /organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strann="AX4"
/db_xref="taxon.44689"
/clone="SiE629"
/dev_stage="slug"
/clone_lib="Dictyostelium discoideum sa 105 c 132 g 235 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               713
46
21
21
37
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaGluLeuGlyIleProAlaGluAspSerTyrLeu---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuArgGlnLeuGlyArgArgGluVal 197
                                                                                           Institute of Biological Sciences
University of Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-613-486-15 (1-198) x AU034876 (1-713)
(6), 335-340 (1998)
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                    Contact: Hideko Urushihara
```

us-09-613-486-15.rst

~

Page

```
EST 19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids; campanulids. Asterales; Asteraceae, Asteroideae; Helianthus.

1 (Dases I to 634)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolhman, C., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Agckson, L. and Bradford, K., Zhou, Y., Lai, Z., Lettuce and Sunflower ESTS from the Compositae Genome Project
                                                                                                                      222 TITGCAGAITICAICGCIGICAAAGIIICAAGTCAICCAGICTAIGAICCAAICTCAAI 163
                               149 AlaAlaAspPheLeuGlyThrCysProLysLeuSerGluLeuGlnGlnSerArgLysMet 168
                                                                                                 169 PheAlaSerMetTyrAlaLeuLysThrGluGlyGlyValValAsnThrProValSerAsn 188
333 ---GAAGGTGGTGAACCTGTAACACCATCATATAAGATTTTGTCAATGGCAACTATTAAC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Alexander Kozik (R.W.Michelmore)
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-9659
Eax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail:ucdavis.edu]
                                                                                                                                                                                                                                               654 bp mRNA linear EST 19-AUG-20
OHB17G04.yg.abl OH ABCDI sunflower RHA801 Helianthus annuus CDNA
clone CHB17G04, mRNA sequence.
                                                               276 GGTGCAAAGGCATTGGGTATCGATGATAAGTTGGTTCACTTCAAATTGGTAAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   654
41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Helianthus annuus"
                                                                                                                                                                                                                                                                                                                                                                        Helianthus annuus (common sunflower)
Helianthus annuus
                                                                                                                                                                   189 LeuArgGlnLeuGlyArgArgGluVal 197
                                                                                                                                                                                                   162 TTAGTTTATGTTGGTACTAATCATGTC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: QHB17 row: G column: 04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://compgenomics.ucdavis.edu/
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4232"
/clone="QHB17G04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="RHA801"
                                                                                                                                                                                                                                                                                                                                      BQ916284.1 GI:22315065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.24
85.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scores:
                                                                                                                                                                                                                                                 BQ916284
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
CRGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scarce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment
                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                               g
                                                                                                                               CD
                                                                                                                                                                 ò
                                                                                                                                                                                                   S
                              ò
                                                                                               \delta
                                               EST 08-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ThrAsnLysLeuArgThrPheGlyArgThrPheThr 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 GluAlaTyrValAspPheCysLeAlaTyrLysHisLysLeuProGlnLeuAsnAlaAla 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   663 GAAGAGGTTAAGGGGTAAGAGACCAATTGAGAGATTGAGAGATTTGGGAGTATTA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 GluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPheGlyLeu 52
                                               linear EST O8-мдк-zv.
dary, CF Dictyostelium
                                                                                            /sex="mat A"
/dev_stage="Culmination stage"
/clone_lib="Dictyostellum discoideum cDNA library, CF"
| 139 c 104 g 264 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 LeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLysValGlnArgAlaAspSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 ValllePheSerAsnSerPheGlyGluArgAsnValValVaiThrGluGlyAspLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 GTTGGTACTGATTCTGCCGCTAGTAATGATGATTTAGATATGTTGGGTGAATTACGTACT
                                            BJ376355
BJ376355 Dictyostelium discoideum cDNA library, C discoideum cDNA clone ddc28n02 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 LysValLeuAspGlyCysAlaProLeuThrArgPhe-----
                                                                                                                                                                                                                                                                                                                                                                                                                  1. 751.
/organism="Dictyostelium discoideum"
/mol_type="manA"
/strafin="AAX4"
/db xref="taxon:44689"
/clone="ddc28n02"
                                                                                                                                                                                                                                                                               Contract: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-854C, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              751
21
85
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 AlaGluLeuGlyIleProAlaGluAspSerTyrLeu---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-613-486-15 (1-198) x BJ376355 (1-751)
                                                                                                                                                                                                                                                                                                                                                                                    Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.36
85.50
35.45$
24.34$
8.63$
                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rcent Similarity:
st Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ignment Scores:
ed. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ery Match:
                                                                                            CCESSION
CRSION
CYWCRDS
CURCE
CRGANISM
            SULT 9
376355/c
                                            CUS
FINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SE COUNT
                                                                                                                                                                                             JFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                               COURNAL
                                                                                                                                                                                                                                                                                                                                                                                                      ATURES
```

IGIN

ore:

us-09-613-486-15.rst

```
/...gul type="mRNA"
/mol type="mRNA"
/cullivar="Salinas"
/dub xref="taxon.4236"
/clone="QGA7M01"
/lab host="E.coli"
/lab host="E.coli"
/lone="Yecror: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 GTTGAAGTTGTGACGCCTGAAGAACATTTGGGGGATGTGATTGGGGGATTTGAATTCGGGA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysvalLeuAspGlyCysAlaProLeuThr-----ArgPheThrAsnLysLeuArg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ThrPheGlyArg---ThrPheThrGluAlaTyrValAspPheCysIleAlaTyr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
        Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

Email: akozik@avgc.org [michelmore@vegmail.ucdavis.edu]

Emoil: akozik@avgc.org [Ca_Contigatorg.edu]

Endongs to contig QG_CA_Contigatorg.see http://cgpdb.ucdavis.edu/

for details.

Plate: QGA7 row: M column: 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GITTTGACCGAT---GGGTCCTACCATGTTGACTCCAGTGTCCTTGCGTTCCAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------TyrLeuAla-----AlaAspPheieuGlyThrCys 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VallieThrAspAlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPheGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuLeuTyrAlaLeuAlaAlaArgThrThrSerProLys-----ValGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AsnSerPheGlyGluArgAsnValValThrGluGlyAspleuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----CTGGCAGCACGAGGGGCGTTTCGGGAAGGTGTT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAG LIBEGG ABCDI lettuce salinas
TAG_TISSUE=shoots environmental stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 610
50
23
47
59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-613-486-15 (1-198) x BQ848646 (1-610)
                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_SEQ=TCGCAACGGG"
_104 c 175 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.35
84.50
40.78
27.93
8.53
                                                                                                                                                           1. .610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
D3:
                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
CRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \ddot{\sigma}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \dot{\varsigma}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \dot{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIO bp mRNA linear EST 14-AUG-2002 GGATMO1.yg.abi QG_ABCDI lettuce salinas Lactuca sativa cDNA clone QGATMO1, mRNA sequence. BQ448646 BQ448646 GI:22234115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryotes Varidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioldeae; Cichorioldeae; Lactuca.

1. (bases i to 610)

Nozik, A. Whichelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Zieg, J., Elison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ETS from the Compositae Genome Project http://compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142
                                                                                                                                                                                                                                                                    83 AsnValValValThrGluGlyAspLeuLysLysValLeuAspGlyCysAlaProLeuThr 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 AlaGluAsp-----SerTyrLeuAlaAlaAspPheLeuGlyThrCysProLysLeuSer 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 GluLeuGlnGlnSerArgLysMetPheAlaSerMetTyrAlaLeuLysThrGluGlyGly 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             532
                                                                                                                                                         30
                                                                                                                                                                                              73
                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                     31 GluyalGluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPhe 50
                                                                                                                                                                                   il AsnLeuVallleThrAspAlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAla
                                                                                                                                                                                                                                                                                                                           -ThrThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                      200 GIGCCGAITGGTTCGGCAGACGTTCGGGCGGTTATAGCAGCGGCAGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 -----AGGGTTCAGAGGAAAGGAAAACACTTTTGTTGGGTGTTCTTGATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 CysileAlaTyrLysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIlePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 TTGAGACGGATCAAGGAAGATGTTAAAGAGGTAAACGCGGGACTAGAGTGTGGTATCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413 GITGAIGACTITAATGAATGGGAAGGTGAATGTAATCGAAGCTTTTAATTCCATTCAG
                                                                                                                                                                                                                                                                                                                                                                                                        64 ProLysValGlrArgAlaAspSerAspValllePheSerAsnSerPheGlyGlu---Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 ArgPheThrAsnLysLeuArgThrPheGlyArgThrPheThrGluAlaTyrValAspPhe
                                                                                                                                                                                                                                                                                                                                                              140 GATCTTCTTGATGATGCGCGAGCGCAATGGAGGGACTACTAGACCCTGTTGAGGATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 GGATGCATGGTGACTGAGGGA-----AAAGTAACAAAAGATTGCGGAGTT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
          31.
889
689
6
        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                    51 GlyLeuleuTyrAlaLeuAlaAlaArg-----
                                                                      Gaps:
                                                                                                             -09-613-486-15 (1-198) x BQ916284 (1-654)
    39,78%
22.65%
8.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactuca sativa
rcent Similarity:
st Local Similarity:
ery Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         533 ATC 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 Val 181
```

SULT 11 848646 CUS FINITION

CESSION

RSION YWORDS

URCE

FERENCE

JOURNAL

MMENT

TITLE

```
GluLysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPheGlyLeu 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:55670"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar="Landrace"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="751/1501"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG526441.1 GI:16949914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stevia rebaudiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stevia rebaudiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
                                         191
                                                                              53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
CRGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCITINITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
BG526441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                          õ
                                                                                                           dC
                                                                                                                                                  ò
                                                                                                                                                                                      qq
                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                dC
                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                       QC.
                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Lab hose = "E.coli"
/ Come lib="GG EFGH' lettuce serriola"
/ Come lib="GG EFGH' lettuce serriola"
/ Come lib="GG EFGH' lettuce serriola"
/ Lobe = "Vector: pBRCDNASfiAs; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. CDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_INSHECDEFCHALDELECHEMICAL Induction.

TAG_INSHECTIONAL Induction.
                                                                                            mRNA linear EST 21-AUG-2062 serriola Lactuca sativa cDNA clone
                                                                                                                                                                                                                                                                                        Cichoriaes; Lactuca.

1 (bases 1 to 61.)

Kozik, A., Miccelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Eilison, P., Kolkman, J., Slabaudh, M.S., Livingston, K., Zhou, Y., Eilison, Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project
Unpublished
                                                                                                                                                                                                         Lactuca sativa
Lactuca sativa
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 VallleThrAspAlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGluVal 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
12-11 - (530) - 752 - 9659
Fax: 1 - (530) - 752 - 9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
611
23
47
59
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Lactuca sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                            BQ984758 61: bp
QGESA05.rg.abl QG_EFGHJ lettuce
QGESA05, mRNA sequence.
BQ984758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: QGE5 row: A column: 05.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGE5A05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -09-613-486-15 (1-198) x BQ984758 (1-611)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_SEQ=TGTAGCCGGG"
                                                                                                                                                                  BQ984758.1 GI:22402283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.35
84.50
40.78%
27.93%
8.53%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rcent Similarity:
st Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ed. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNT
                                                                                                             FINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                           ORGANISM.
                                                                                                                                                                                                                                                                                                                       FERENCE
                                                                                                                                                    CESSION
                                                                                                                                                                    RSION
YWORDS
                                                                            984758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATURES
                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ore:
```

```
BG526441 632 bp mRNA linear EST 16-NOV-2001 61-95 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="field_grown, mid-size"
/lab_host="E. coli strain XLOLR"
/clone lib="Stevia field grown leaf cDNA"
/note="Yector: pBK-CMV, Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed_from polyA+ enriched mRNA from field grown leaves. Mid-size actively growing leaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 -----ThrPheGlyArg---ThrPheThrGluAlaTyrValAspPheCysIleAlaTyr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 LysHisLysLeuProGlnLeuAsnAlaAlaAlaGluLeuGlyIleProAlaGluAspSer 146
                                                                                                                          263 GTTGAAGTTGTGACGCCTGAAGAACATTTGGGGGATGTGATTTGGGGGATTTTGAATTCGAGA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 AGAGGCCACATTAATAGCTTTGGTGATAAG-------CCTGGTGGACTT--- 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 AAGGTGGTGGATTCTTTGGTCCCACTTGCGGAAATGTTTCAGTATGTGAGTACTTTAAGG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              485 CAACATATTCAGAACCAGCTTTCTGCTGCTAAAGAAGAAGCTGTGGCAGCTTGATCTTCA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids, campanulids, Asterales, Asteraceae, Asteroideae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eupatorieae, Stevia.

1 (bases 1 to 632)

Brandle,J.E., Richman,A., Swanson,A.K. and Chapman,B.P.

Leaf ESTs from Stevia rebaudiana: A resource for gene discovery diterpene synthesis

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 ------TyrLeuAla-----AlaAspPheLeuGlyThrCys 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     545 TCTTCATCTTTGTGCTATTAATGATAGGGGAATTTTCTGATTTTCACTTCATATGT 601
                                                                             LeuLeuTyrAlaLeuAlaAlaAiaArgThrThrSerProLys-----ValGlnArg
                                                                                                                                                                                                                                                                                                                                                                                           ------AsnSerPheGlyGluArgAsnValValThrGluGiyAspLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 LysValLeuAspGlyCysAlaProLeuThr ----- ArgPheThrAsnLysLeuArg
                                                                                                                                                                                                                                    -----SerAspValllePheSer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Jim Brandle
Genomics and Biotechnology
Agriculture and Agri-Food Canada - SCPFRC
Agriculture and Agri-Food Contacto, CANADA, NSV 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: brandleje@em.agr.ca
Seq primer: T3 promoter primer.
Location/Qualifiers
-----craccaccaccaccaccarrrcccaaaccrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Stevia rebaudiana"
```

IGIN

ore:

```
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-613-486-15 (1-198) x BG523153 (1-648)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.56
84.50
40.57%
27.43%
8.53%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                            AUTHORS
TITLE
                                              REFERENCE
                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
were collected and pooled from several plants and frozen immediately after harvesting in liquid nitrogen. The CDNA was prepared using an Xhol-poly(dT) linker-primer. An EcoRI adapter was lighted to the blunt end cDNA and the products were digested with EcoRI and Xhol enabling directional cloning into the lambda ZAP Express vector. The library was amplified using the bost strain XLI-Blue MRF'. Mass excision of the library was performed to obtain pBK-CMV phagemid clones in the host strain XLOLR. Single pass DNA sequencing was performed using the T3 promoter primer: 5' ATTAACCTCATAAAGGGA 3' This library was constlucted by Alex Alchman." I others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648 bp mRNA linear EST 16-NOV-2001
leaf cDNA Stevia rebaudiana cDNA 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stevia rebaudiana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 LeuAspGlyCysAlaProLeuThr-----ArgPheThrAsnLysLeuArg---- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                       -----Vaiile 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 ThrAspAlaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGluValGluLys 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 ------AGGAAAGCGGGTCCCAAGATTTGGAACCCATATGAGAGTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 ThrPheG'yArg---ThrPheThrGluAlaTyrValAspPheCysIleAlaTyrLysHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 MetLeuValGinLysGlyAlaProAsnGluGlyIleGluValValPheGlyLeuLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 TyralaLeuAlaAlaArgThrThrSerProLys------ValGlnArgAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 GTTGTGACACCTGAAGAACATTTGGGTGATGTTATTGGTGATTTTGAATTCTAGAAGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 GTGGATTCACTTGTGCCACTAGCAGAAATGTTTCAATATGTGAGTACGTTAAGAGGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 -----AsnSerPheGiyGluArgAsnValValValThrGluGlyAspLeuLysLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 ----------SerAspValilePheSer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 LysLeuProGlnieuAsnAlaAlaAlaGluLeuGlyIleProAla 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           470 ATTCAGAACCAACTTTCTGCTGCCAAAGAAGAAGCAGTTACAGCT 514
                                                                                                                                                                                                                                                                                                                                                                                                                                   GlubeuMetSerAspSerAspbeuSerAspbeu-----
                                                                                                                                                                                                                                                                                632
48
23
47
57
                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                 -09-613-486-15 (1-198) x BG526441 (1-632)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG523153
29-48 Stevia field grown
seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:16946562
                                                                                                                                                                                                                                                                                2.47
84.50
40.57%
27.43%
8.53%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST.
Stevia rebaudiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG523153.1
                                                                                                                                                                                                                                                                                                              rcent Similarity:
st Local Similarity:
ery Match:
                                                                                                                                                                                                                ಹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG523153
                                                                                                                                                                                                                                                                 ignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSION
YWORDS
URCE
ORGANISM
                                                                                                                                                                                                                                                                                 ed. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FINITION
                                                                                                                                                                                                                SE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SULT 14
523153
CUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CESSION
```

```
Standle, Jean Stevia repairs and Chapmar, B.F.

Estandle, J.E., Richman, A., Swanson, A.K. and Chapmar, B.F.

Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in diterpene synthesis
Unpublished (2001)
Contact: Jim Brandle
Genomics and Biotechnology
Agriculture and Agri-Food Canada - SCPFRC
1391 Sandford St., London, Ontario, CANADA, N5V 4T3
Fax: 519 457 1470
Fax: 519 457 1397
Email: brandleje@em.agr.ca
Seq primer: 73 proncter primer.
                                                <u>...</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGTCAATGTCTAATGGAGTACTCGCGGGTTTCCCTGTTGTTGACCTTCGTGCGGTGTTG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -------AGGAAAGCGGGTCCCAAGATTTTGGAACCCATTATGAGAGTTGAA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 GTTGTGACACCTGAAGAACATTTGGGTGATGTTATTGGTGATTTTGAATTCTAGAAGAGAGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThraspalaSerSerLeuAsnGlyValAspLysLysLeuLeuSerAlaGluValGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyralaieualaalaargThrThrSerProLys------ValGlmArgAlaasp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SerAspyalllePheSer----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluLeuMetSerAspSerAsnLeuSerAsnLeu--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648
23
47
57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
```

. 8	77AsmSerPheGlyGluArgAsmValValUalThrGluGlyAspLeuLysLysVal 94	Score: Percent Similarit Best Local Simila
-	LeuAspGlyCysAlaproLeuThrArgPheThrAsnLysLeuArg	US: US-09-613-486-15
e o	368 GTGGATTCACTTGTGCCCACTAGCAGAAATGTTTCAATATGTGAGTACGTTAAGAGGAATG 427	Cv 13 Val
el :	ThrPheGlyArgThrPheThrGluAlaTyrValAspPheCysIleAlaTyrLysHis	172
4.	428 ACAAAAGGTCGAGCATCTTACACTATGCAACTAGGAAATTCGATGTGGTACCTCAACAC 487	Oy 33 Glu
I 4	129	Db 226
	700 17000701100700000000000000000000000	Qy 53 Leu
99301 4 CHS	R0991014 FQT 7: AND AND 1: ALC: 2002	259
FINITION	GGF27F14, FRNA sequence.	Oy 69 Ala
CESSION RSION	BQ993014 BQ993014.1 GI:22412549	Db 298 GTT
YWORDS URCE	EST. Lactuca sativa	Oy 77
ORGANISM	Sactica sativa Enkarvora: Viridiolantae: Streptonbyta: Embryonbyta: Tranheombyta:	Db 358 AGA
	Spermatophyta; Magnollophyta; endicotyledons; core endicots; asterfats; carpanulids; Asterales; Asteraceae; Cichotioideae;	Oy 93 Lys
PERENCE	1 (bases 1 to 695)	, ,
AUTHORS	<pre>Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,J., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison</pre>	Oy 110
	, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, J., and Bradford K	DD 460 GGA
TITLE	Lettuce and Sunflower ESTs from the Compositae Genome Project	0y 127 Lys
JOURNAL	nttp://compgenomics.ucdavis.edu/ Unpublished	::: CD 250 CAA
MMENT	Contact: Alexander Kozik (R.W.Michelmore) Department of Vegetable Crops, R.W.Michelmore Lab	Oy 147
	University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA	TOT 089 TCT
	Tel: 1-(530)-742-1742 Fax: 2-(530)-752-9659	;
	Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] helongs to contin 02 Ca Continils see http://cmdh.ucdavis.edu/	Search completed:
	Contains to contain the contains the contain	1
SATURES	Location/Qualifiers	
source	: 1695 /organism="Lactuca sativa" /mol_type="mRNA" /cullivar="L.serriola"	
	/db_xref="taxon:4236" /clone="QGF27F14"	
	/lab host="E.col"	
	/note=-vector: parcunatina; ine libiary was constructed from 10 different sources of RNA from a single genotype. Separate con%s were generated using primers that	
	incorporated unique 5' and 3' tags to distinguish each source of RNA. corks were then pooled, size-fractionadiative cloned into a custom medium-copy vector and	
	transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/	
ASE COUNT	189 a 115 c 197 g 194 t	

695

Length:

2.84

```
----ThrPheGlyArg---ThrPheThrGluAlaTyrValAspFheCyslleAlaTyr 126
                                                                                                                                                                                                                                                                                                                                                                                                SHisLysLeuProGlnieuAsnAlaAlaAlaGluieuGlyIleProAlaGluAspSer 146
                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAAGTTGTGACCCCTGAAGAACATTTGGGGGATGTGTTTGGGGGATTTGAATTCGAGA 357
                                                                                                                                                                                                                                                                                                  uLeuTyrAlaLeuAlaAlaArgThrThrSerProLys-----ValGlrArg 68
                                                                                                                                                                                                                                                                                    ------AsnSerPheGlyGluArgAsnValValValThrGluGlyAspLeuLys 92
                                                                                                                                            uLysMetLeuValGlnLysGlyAlaProAsnGluGlyIleGluValValPheGly5eu 52
                                                                                                                                                                                                                                       aAsp-------76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TyrLeuAla-----AlaAspPheLeuGlyThrCys 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50
23
47
59
13
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i: November 8, 2003, 31:33:55 secs
                                                                      (1-198) x BQ993014 (1-695)
 84.50
40.78%
27.93%
8.53%
              ity:
Larity:
```